

A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM THE
GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA LIBRARY
APPLICATION TO THE DETECTION OF MYCOBACTERIA

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I. Background of the invention

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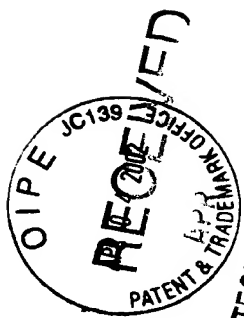
[001] The present invention pertains to a method for isolating a polynucleotide of interest that is present in the genome of a mycobacterium strain and/or is expressed by said mycobacterium strain and that is absent or altered in the genome of a different mycobacterium strain and/or is not expressed in said different mycobacterium strain, said method comprising the use of at least one clone belonging to a genomic DNA library of a given mycobacterium strain, said DNA library being cloned in a bacterial artificial chromosome (BAC). The invention concerns also polynucleotides identified by the above method, as well as detection methods for mycobacteria, particularly *Mycobacterium tuberculosis*, and kits using said polynucleotides as primers or probes. Finally, the invention deals with BAC-based mycobacterium DNA libraries used in the method according to the invention and particularly BAC-based *Mycobacterium tuberculosis* and *Mycobacterium bovis* BCG DNA libraries.

[002] Radical measures are required to prevent the grim predictions of the World Health Organisation for the evolution of the global tuberculosis epidemic in the next century becoming a tragic reality. The powerful combination of genomics and bioinformatics is providing a wealth of information about the etiologic agent, *Mycobacterium tuberculosis*, that will facilitate the conception and development of new therapies. The start point for genome sequencing was the integrated map of the 4.4 Mb circular chromosome of the widely-used, virulent reference strain, *M. tuberculosis* H37Rv and appropriate cosmids were subjected to systematic shotgun sequence analysis at the Sanger Centre.

[003] Cosmid clones (Balasubramanian et al., 1996; Pavelka et al., 1996) have played a crucial role in the *M. tuberculosis* H37Rv genome sequencing project. However, problems such as under-representation of certain regions of the chromosome, unstable inserts and the relatively small insert size complicated the production of a comprehensive set of canonical cosmids representing the entire genome.

II. Summary of the invention

[004] In order to avoid the numerous technical constraints encountered in the state of the art, as described hereabove, when using genomic mycobacterial DNA libraries constructed in cosmid clones, the inventors have attempted to realize genomic



mycobacterial DNA libraries in an alternative type of vectors, namely Bacterial Artificial Chromosome (BAC) vectors.

[005] The success of this approach depended on whether the resulting BAC clones could maintain large mycobacterial DNA inserts. There are various reports describing the successful construction of a BAC library for eucaryotic organisms (Cai et al., 1995; Kim et al., 1996; Misumi et al., 1997; Woo et al., 1994; Zimmer et al., 1997) where inserts up to 725 kb (Zimmer et al., 1997) were cloned and stably maintained in the *E. coli* host strain.

[006] Here, it is shown that, surprisingly, the BAC system can also be used for mycobacterial DNA, as 70% of the clones contained inserts in the size of 25 to 104 kb.

[007] This is the first time that bacterial, and specifically mycobacterial, DNA is cloned in such BAC vectors.

[008] In an attempt to obtain complete coverage of the genome with a minimal overlapping set of clones, a Bacterial Artificial Chromosome (BAC) library of *M. tuberculosis* was constructed, using the vector pBeloBAC11 (Kim et al., 1996) which combines a simple phenotypic screen for recombinant clones with the stable propagation of large inserts (Shizuya et al., 1992). The BAC cloning system is based on the *E. coli* F-factor, whose replication is strictly controlled and thus ensures stable maintenance of large constructs (Willems et al., 1987). BACs have been widely used for cloning of DNA from various eucaryotic species (Cai et al., 1995; Kim et al., 1996; Misumi et al., 1997; Woo et al., 1994; Zimmer et al., 1997). In contrast, to our knowledge this report describes the first attempt to use the BAC system for cloning bacterial DNA.

[009] A central advantage of the BAC cloning system over cosmid vectors used in prior art is that the F-plasmid is present in only one or a maximum of two copies per cell, reducing the potential for recombination between DNA fragments and, more importantly, avoiding the lethal overexpression of cloned bacterial genes. However, the presence of the BAC as just a single copy means that plasmid DNA has to be extracted from a large volume of culture to obtain sufficient DNA for sequencing and it is described here in the examples a simplified protocol to achieve this.

[010] Further, the stability and fidelity of maintenance of the clones in the BAC library represent ideal characteristics for the identification of genomic differences possibly responsible for phenotypic variations in different mycobacterial species.

[011] As it will be shown herein, BACs can be allied with conventional hybridization techniques for refined analyses of genomes and transcriptional activity from different mycobacterial species.

[012] Having established a reliable procedure to screen for genomic polymorphisms, it is now possible to conduct these comparisons on a more systematic basis than in prior art using representative BACs throughout the chromosome and genomic DNA from a variety of mycobacterial species.

[013] As another approach to display genomic polymorphisms, the inventors have also started to use selected H37Rv BACs for "molecular combing" experiments in combination with fluorescent *in situ* hybridization (Bensimon et al., 1994; Michalet et al., 1997). With such techniques the one skilled in the art is enabled to explore the genome of mycobacteria in general and of *M. tuberculosis* in particular for further polymorphic regions.

[014] The availability of BAC-based genomic mycobacterial DNA libraries constructed by the inventors have allowed them to design methods and means both useful to identify genomic regions of interest of pathogenic mycobacteria, such as *Mycobacterium tuberculosis*, that have no counterpart in the corresponding non-pathogenic strains, such as *Mycobacterium bovis* BCG, and useful to detect the presence of polynucleotides belonging to a specific mycobacterium strain in a biological sample.

[015] By a biological sample according to the present invention, it is notably intended a biological fluid, such as plasma, blood, urine or saliva, or a tissue, such as a biopsy.

[016] Thus, a first object of the invention consists of a method for isolating a polynucleotide of interest that is present in the genome of a mycobacterium strain and/or is expressed by said mycobacterium strain and that is absent or altered in the genome of a different mycobacterium strain and/or is not expressed in said different mycobacterium strain, said method comprising the use of at least one clone belonging to a genomic DNA library of a given mycobacterium strain, said DNA library being cloned in a bacterial artificial chromosome (BAC).

[017] The invention is also directed to a polynucleotide of interest that has been isolated according to the above method and in particular a polynucleotide containing one or several Open Reading Frames (ORFs), for example ORFs encoding either a polypeptide involved in the pathogenicity of a mycobacterium strain or ORFs encoding Polymorphic Glycine Rich Sequences (PGRS).

[018] Such polynucleotides of interest may serve as probes or primers in order to detect the presence of a specific mycobacterium strain in a biological sample or to detect the expression of specific genes in a particular mycobacterial strain of interest.

[019] The BAC-based genomic mycobacterial DNA libraries generated by the present inventors are also part of the invention, as well as each of the recombinant BAC clones and the DNA insert contained in each of said recombinant BAC clones.

[020] The invention also pertains to methods and kits for detecting a specific mycobacterium in a biological sample using either at least one recombinant BAC clone or at least one polynucleotide according to the invention, as well as to methods and kits to detect the expression of one or several specific genes of a given mycobacterial strain present in a biological sample.

III. Brief description of the Figures.

[021] In order to better understand the present invention, reference will be made to the appended figures which depicted specific embodiments to which the present invention is in no case limited in scope with.

[022] **Figures 1A and 1B :** PCR-screening for unique BAC clones with specific primers for 2 selected genomic regions of the H37Rv chromosome, using 21 pools representating 2016 BACs (Figure 1A) and sets of 20 subpools from selected positive pools (Figure 1B).

[023] **Figure 2 :** Pulsed-field gel electrophoresis gel of *DraI*-cleaved BAC clones used for estimating the insert sizes of BACs.

[024] **Figure 3 :** Minimal overlapping BAC map of *M. tuberculosis* H37Rv superimposed on the integrated physical and genetic map established by Philipp et al. (18). Y- and I- numbers show pYUB328 (2) and pYUB412 (16) cosmids which were shotgun sequenced during the H37Rv genome sequencing project. Y-cosmids marked with * were shown in the integrated physical and genetic map (18). Rv numbers show the position of representative BAC clones relative to sequenced Y- and I- clones. Squared Rv numbers show BACs which were shotgun sequenced at the Sanger Centre.

[025] **Figures 4A and 4B :** Ethidium bromide stained gel (Figure 4A) and corresponding Southern blot (Figure 4B) of *EcoRI* and *PvuII* digested Rv58 DNA hybridized with ³²P labeled genomic DNA preparations from *M. tuberculosis* H37Rv, *M. bovis* ATCC 19210 and *M. bovis* BCG Pasteur.

[026] **Figure 5 :** Organisation of the ORFs in the 12.7 kb genomic region present in *M. tuberculosis* H37Rv but not present in *M. bovis* ATCC 19210 and *M. bovis* BCG

Pasteur. Arrows show the direction of transcription of the putative genes. Positions of *EcoRI* and *PvuII* restriction sites are shown. Vertical dashes represent stop codons. The 11 ORFs correspond to the ORFs MTCY277.28 to MTCY277.38 / accession number Z79701 -EMBL Nucleotide Sequence Data Library. The junction sequences flanking the polymorphic region are shown.

[027] **Figure 6** : Variation in the C-terminal part of a PE-PGRS open reading frame in *M. tuberculosis* strain H37Rv relative to *M. bovis* BCG strain Pasteur.

[028] The numbers on the right side of the Figure denote the position of the end nucleotides, taking as the reference the *M. tuberculosis* genome.

[029] **Figure 7** : Polynucleotide sequence next to the HindIII cloning site in the BAC vector pBeloBAC11 (Kim et al., 1996) used to clone the inserts of the BAC-based myobacterial genomic DNA library according to the invention.

[030] NotI : location of the NotI restriction sites.

[031] Primer T7-BAC1 : nucleotide region recognized by the T7-BAC1 primer shown in Table 1.

[032] T7 promoter: location of the T7 promoter region on the pBeloBac11 vector.

[033] Primer T7-Belo2 : nucleotide region recognized by the T7-Belo2 primer shown in Table 1.

[034] Hind III : the HindIII cloning site used to clone the genomic inserts in the pBeloBAC11 vector.

[035] SP6-Mid primer: nucleotide region recognized by the SP6 Mid primer shown in Table 1.

[036] SP6-BAC1 primer : nucleotide region recognized by the SP6 BAC1 primer shown in Table 1.

[037] SP6 promoter: location of the SP6 promoter region on the pBeloBac11 vector.

IV. Detailed description of the preferred embodiments.

[038] As already mentioned hereinbefore, the present invention is directed to a method for isolating a polynucleotide of interest that is present in the genome of a mycobacterium strain and/or is expressed by said mycobacterium strain and that is absent or altered in the genome of a different mycobacterium strain and/or is not expressed in said different mycobacterium strain, said method comprising the use of at least one clone

belonging to a genomic DNA library of a given mycobacterium strain, said DNA library being cloned in a bacterial artificial chromosome (BAC) type vector.

[039] For this purpose, the inventors have constructed several BAC-based mycobacterial genomic DNA libraries that may be used in order to perform the above described method.

[040] Because it is the first time that mycobacterial genomic DNA has been successfully cloned in BAC type vectors, and because these DNA libraries are then novel and nonobvious, an object of the present invention consists in a mycobacterial genomic DNA library cloned in such a BAC type vector.

[041] As an illustrative example, a BAC-based DNA library of *Mycobacterium tuberculosis* has been realized. Forty-seven cosmids chosen from the integrated map of the 4.4 Mb circular chromosome (Philipp et al., 1996a) were shotgun-sequenced during the initial phase of the H37Rv genome sequence project. The sequences of these clones were used as landmarks in the construction of a minimally overlapping BAC map. Comparison of the sequence data from the termini of 420 BAC clones allowed us to establish a minimal overlapping BAC map and to fill in the existing gaps between the sequence of cosmids. As well as using the BAC library for genomic mapping and sequencing, we also tested the system in comparative genomic experiments in order to uncover differences between two closely related mycobacterial species. As shown in a previous study (Philipp et al., 1996b), *M. tuberculosis*, *M. bovis* and *M. bovis* BCG, specifically BCG Pasteur strain, exhibit a high level of global genomic conservation, but certain polymorphic regions were also detected. Therefore, it was of great interest to find a reliable, easy and rapid way to exactly localize polymorphic regions in mycobacterial genomes using selected BAC clones. This approach was validated by determining the exact size and location of the polymorphisms in the genomic region of *DraI* fragment Z4 (Philipp et al., 1996b), taking advantage of the availability of an appropriate BAC clone covering the polymorphic region and the H37Rv genome sequence data. This region is located approximately 1.7 Mb from the origin of replication.

[042] The Bacterial Artificial Chromosome (BAC) cloning system is capable of stably propagating large, complex DNA inserts in *Escherichia coli*. As part of the *Mycobacterium tuberculosis* H37Rv genome sequencing project, a BAC library was constructed in the pBeloBAC11 vector and used for genome mapping, confirmation of sequence assembly, and sequencing. The library contains about 5000 BAC clones, with inserts ranging in size from 25 to 104 kb, representing theoretically a 70 fold coverage of

the *M. tuberculosis* genome (4.4 Mb). A total of 840 sequences from the T7 and SP6 termini of 420 BACs were determined and compared to those of a partial genomic database. These sequences showed excellent correlation between the estimated sizes and positions of the BAC clones and the sizes and positions of previously sequenced cosmids and the resulting contigs. Many BAC clones represent linking clones between sequenced cosmids, allowing full coverage of the H37Rv chromosome, and they are now being shotgun-sequenced in the framework of the H37Rv sequencing project. Also, no chimeric, deleted or rearranged BAC clones were detected, which was of major importance for the correct mapping and assembly of the H37Rv sequence. The minimal overlapping set contains 68 unique BAC clones and spans the whole H37Rv chromosome with the exception of a single gap of ~ 150 kb. As a post-genomic application, the canonical BAC set was used in a comparative study to reveal chromosomal polymorphisms between *M. tuberculosis*, *M. bovis* and *M. bovis* BCG Pasteur, and a novel 12.7 kb segment present *M. tuberculosis* but absent from *M. bovis* and *M. bovis* BCG was characterized. This region contains a set of genes whose products show low similarity to proteins involved in polysaccharide biosynthesis. The H37Rv BAC library therefore provides the one skilled in the art with a powerful tool both for the generation and confirmation of sequence data as well as for comparative genomics and a plurality of post-genomic applications.

[043] The above described BAC-based *Mycobacterium tuberculosis* genomic DNA library is part of the present invention and has been deposited in the Collection Nationale de Cultures de Microorganismes (CNCM) on November 19, 1997 under the accession number 1-1945.

[044] Another BAC-based DNA library has been constructed with the genomic DNA of *Mycobacterium bovis* BCG, Pasteur strain, and said DNA library has been deposited in the Collection Nationale de Cultures de Microorganismes (CNCM) on June 30, 1998 under the accession number I-2049.

[045] Thus, as a specific embodiment of the above described method for isolating a polynucleotide of interest said method makes use of at least one BAC-based DNA library that has been constructed from the genomic DNA of *Mycobacterium tuberculosis*, more specifically of the H37Rv strain and particularly of the DNA library deposited in the accession number 1-1945.

[046] In another specific embodiment of the above described method for isolating a polynucleotide of interest said method makes use of at least one BAC-based

DNA library has been constructed from the genomic DNA of *Mycobacterium bovis* BCG, more specifically of the Pasteur strain and particularly of the DNA library deposited in the accession number I-2049.

[047] In more details, the method according to the invention for isolating a polynucleotide of interest may comprise the following steps :

[048] a) isolating at least one polynucleotide contained in a clone of a BAC-based DNA library of mycobacterial origin;

[049] b) isolating:

[050] - at least one genomic or cDNA polynucleotide from a mycobacterium, said mycobacterium belonging to a strain different from the strain used to construct the BAC-based DNA library of step a); or alternatively

[051] - at least one polynucleotide contained in a clone of a BAC-based DNA library prepared from the genome of a mycobacterium that is different from the mycobacterium used to construct the BAC-based DNA library of step a);

[052] c) hybridizing the at least one polynucleotide of step a) to the at least one polynucleotide of step b);

[053] d) selecting the at least one polynucleotide of step a) that has not formed a hybrid complex with the at least one polynucleotide of step b);

[054] e) characterizing the selected polynucleotide.

[055] Following the above procedure, the at least one polynucleotide of step a) may be prepared as follows :

[056] 1) digesting at least one recombinant BAC clone by an appropriate restriction endonuclease in order to isolate the polynucleotide insert of interest from the vector genetic material;

[057] 2) optionally amplifying the resulting polynucleotide insert;

[058] 3) optionally digesting the polynucleotide insert of step 1) or step 2) with at least one restriction endonuclease.

[059] The above method of the invention allows the one skilled in the art to perform comparative genomics between different strains or species of mycobacteria cells, for example between pathogenic strains or species and their non pathogenic strains or species counterparts, as it is the illustrative case for the genomic comparison between *Mycobacterium tuberculosis* and *Mycobacterium bovis* BCG that is described herein in the examples.

[060] Restriction digests of a given clone of a BAC library according to the invention may be blotted to membranes, and then probed with radiolabeled DNA from another strain or another species of mycobacteria, allowing the one skilled in the art to identify, characterize and isolate a polynucleotide of interest that may be involved in important metabolic and/or physiological pathways of the mycobacterium under testing, such as a polynucleotide functionally involved in the pathogenicity of said given mycobacteria for its host organism.

[061] More specifically, the inventors have shown in Example 6 that when restriction digests of a given clone of the BAC library identified by the CNCM accession number 1-1945 are blotted to membranes and then probed with radiolabeled total genomic DNA from, for example, *Mycobacterium bovis* BCG Pasteur, it is observed that restriction fragments that fail to hybridize with the *M. bovis* BCG Pasteur DNA are absent from its genome, hence identifying polymorphic regions between *M. bovis* BCG Pasteur and *M. tuberculosis* H37Rv.

[062] Thus, a further object of the present invention consists in a polynucleotide of interest that has been isolated according to the method described herein before.

[063] In Example 6, a polynucleotide of approximately 12.7 kilobases has been isolated that is present in the genome of *M. tuberculosis* but is absent of the genome of *M. bovis* BCG. This polynucleotide of interest contains 11 ORFs that may be involved in polysaccharide biosynthesis. In particular, two of said ORFs are of particular interest namely ORF6 (MTCY277.33; Rv1511) that encodes a protein that shares significant homology with bacterial GDP-D-mannose dehydratases, whereas the protein encoded by ORF7 (MTCY277.34; Rv1512) shares significant homology with a nucleotide sugar epimerase. As polysaccharide is a major constituent of the mycobacterial cell wall, these deleted genes may cause the cell wall of *M. bovis* BCG to differ from that of *M. tuberculosis*, a fact that may have important consequences for both the immune response to *M. bovis* BCG and virulence. Detection of such a polysaccharide is of diagnostic interest and possibly useful in the design of tuberculosis vaccines.

[064] Consequently, the polynucleotide of interest obtained following the method according to the invention may contain at least one ORF, said ORF preferably encoding all or part of a polypeptide involved in an important metabolic and/or physiological pathway of the mycobacteria under testing, and more specifically all or part of a polypeptide that is involved in the pathogenicity of the mycobacteria under testing,

such as for example *Mycobacterium tuberculosis*, and more generally mycobacteria belonging to the *Mycobacterium tuberculosis* complex.

[065] The *Mycobacterium tuberculosis* complex has its usual meaning, i.e. the complex of mycobacteria causing tuberculosis which are *Mycobacterium tuberculosis*, *Mycobacterium bovis*, *Mycobacterium africanum*, *Mycobacterium microti* and the vaccine strain *Mycobacterium bovis* BCG.

[066] An illustrative polynucleotide of interest according to the present invention comprises all or part of the polynucleotide of approximately 12.7 kilobases that is present in the genome of *M. tuberculosis* but is absent from the genome of *M. bovis* BCG disclosed hereinbefore. This polynucleotide is contained in clone Rv58 of the BAC DNA library I-1945.

[067] Generally, the invention also pertains to a purified polynucleotide comprising the DNA insert contained in a recombinant BAC vector belonging to a BAC-based mycobacterial genomic DNA library, such as for example the I-1945 BAC DNA library.

[068] Advantageously, such a polynucleotide has been identified according to the method of the invention.

[069] Such a polynucleotide of interest may be used as a probe or a primer useful for specifically detecting a given mycobacterium of interest, such as *Mycobacterium tuberculosis* or *Mycobacterium bovis* BCG.

[070] More specifically, the invention then deals with a purified polynucleotide useful as probe or a primer comprising all or part of the nucleotide sequence SEQ ID N° 1.

[071] The location, on the *Mycobacterium tuberculosis* chromosome, of the above polynucleotide of sequence SEQ ID N° 1 has now been ascribed to begin, at its 5' end at nucleotide at position nt 1696015 and to end, at its 3' end, at nucleotide at position nt 1708746.

[072] For diagnostic purposes, this 12.7 kb deletion should allow a rapid PCR screening of tubercle isolates to identify whether they are bovine or human strains. The primers listed in Table I are flanking the deleted region and give a 722 bp amplicon in *M. bovis* or *M. bovis* BCG strains, but a fragment of 13,453 bp in *M. tuberculosis* that is practically impossible to amplify under the same PCR conditions. More importantly, assuming that some of the gene products from this region represent proteins with antigenic properties, it could be possible to develop a test that can reliably distinguish

between the immune response induced by vaccination with *M. bovis* BCG vaccine strains and infection with *M. tuberculosis* or that the products (e.g. polysaccharides) are specific immunogens.

[073] The invention also provides for a purified polynucleotide useful as a probe or as a primer, said polynucleotide being chosen in the following group of polynucleotides :

[074] a) a polynucleotide comprising at least 8 consecutive nucleotides of the sequence SEQ ID N° 1;

[075] b) a polynucleotide whose sequence is fully complementary to the sequence of the polynucleotide defined in a);

[076] c) a polynucleotide that hybridizes under stringent hybridization conditions with the polynucleotide defined in a) or with the polynucleotide defined in b).

[077] For the purpose of defining a polynucleotide or oligonucleotide hybridizing under stringent hybridization conditions, such as above, it is intended a polynucleotide that hybridizes with a reference polynucleotide under the following hybridization conditions.

[078] The hybridization step is realized at 65°C in the presence of 6 x SSC buffer, 5 x Denhardt's solution, 0,5% SDS and 100µg/ml of salmon sperm DNA.

[079] For technical information, 1 x SSC corresponds to 0.15 M NaCl and 0.05M sodium citrate; 1 x Denhardt's solution corresponds to 0.02% Ficoll, 0.02% polyvinylpyrrolidone and 0.02% bovine serum albumin.

[080] The hybridization step is followed by four washing steps :

[081] - two washings during 5 min, preferably at 65°C in a 2 x SSC and 0.1% SDS buffer,

[082] - one washing during 30 min, preferably at 65°C in a 2 x SSC and 0.1% SDS buffer,

[083] - one washing during 10 min, preferably at 65°C in a 0.1 x SSC and 0.1%SDS buffer.

[084] A first illustrative useful polynucleotide that is included in the polynucleotide of sequence SEQ ID N°1 is the polynucleotide of sequence SEQ ID N°2 that corresponds to the Sp6 end-sequence of SEQ ID N°1.

[085] A second illustrative useful polynucleotide that is included in the polynucleotide of sequence SEQ ID N°1 is the polynucleotide of sequence SEQ ID N°3 that corresponds to the T7 end-sequence of SEQ ID N°1, located on the opposite strand.

[086] The polynucleotide of sequence SEQ ID N°1 contains 11 ORFs, the respective locations of which, taking into account the orientation of each ORF on the chromosome, on the sequence of the *Mycobacterium tuberculosis* chromosome, is given hereafter:

[087] - The location of ORF1 is comprised between nucleotide at position nt 1695944 and nucleotide at position nt 1696441.

[088] - The location of ORF2 is comprised between nucleotide at position nt 1696728 and nucleotide at position nt 1697420.

[089] - The location of ORF3 is comprised between nucleotide at position nt 1698096 and nucleotide at position nt 1699892. ORF3 probably encodes a protein having the characteristics of a membrane protein.

[090] - The location of ORF4 is comprised between nucleotide at position nt 1700210 and nucleotide at position nt 1701088.

[091] - The location of ORF5 is comprised between nucleotide at position nt 1701293 and nucleotide at position nt 1702588. ORF5 encodes a protein having the characteristics of a membrane protein.

[092] - The location of ORF6 is comprised between nucleotide at position nt 1703072 and nucleotide at position nt 1704091. ORF6 encodes a protein having the characteristics of a GDP-D-mannose dehydratase.

[093] - The location of ORF7 is comprised between nucleotide at position nt 1704091 and nucleotide at position nt 1705056. ORF7 encodes a protein having the characteristics of a nucleotide sugar epimerase involved in colanic acid biosynthesis.

[094] - The location of ORF8 is comprised between nucleotide at position nt 1705056 and nucleotide at position nt 1705784.

[095] - The location of ORF9 is comprised between nucleotide at position nt 1705808 and nucleotide at position nt 1706593. ORF9 encodes a protein having the characteristics of colanic acid biosynthesis glycosyl transferase.

[096] - The location of ORF10 is comprised between nucleotide at position nt 1706631 and nucleotide at position nt 1707524.

[097] - The location of ORF11 is comprised between nucleotide at position nt 1707530 and nucleotide at position nt1708648. ORF11 encodes a protein similar to a spore coat polysaccharide biosynthesis.

[098] A polynucleotide of interest obtained by the above-disclosed method according to the invention may also contain at least one ORF that encodes all or part of acidic, glycine-rich proteins, belonging to the PE and PPE families, whose genes are often clustered and based on multiple copies of the polymorphic repetitive sequences. The names PE and PPE derive from the fact that the motifs ProGlu (PE, positions 8, 9) and ProProGlu (PPE, positions 7 to 9) are found near the N-terminus in almost all cases. The PE protein family all have a highly conserved N-terminal domain of ~110 amino acid residues, that is predicted to have a globular structure, followed by a C-terminal segment which varies in size, sequence and repeat copy number. Phylogenetic analysis separated the PE family into several groups, the larger of which is the highly repetitive PGRS class containing 55 members whereas the other groups share very limited sequence similarity in their C-terminal domains. The predicted molecular weights of the PE proteins vary considerably as a few members only contain the ~110 amino acid N-terminal domain while the majority have C-terminal extensions ranging in size from 100 up to >1400 residues. A striking feature of the PGRS proteins is their exceptional glycine content (up to 50%) due to the presence of multiple tandem repetitions of GlyGlyAla or GlyGlyAsn motifs or variations thereof.

[099] Like the PE family, the PPE protein family also has a conserved N-terminal domain that comprises ~180 amino acid residues followed by C-terminal segments that vary considerably in sequence and length. These proteins fall into at least three groups, one of which constitutes the MPTR class characterised by the presence of multiple, tandem copies of the motif AsnXGlyXGlyAsnXGly (SEQ ID NO. 730). The second subgroup contains a characteristic, well-conserved motif around position 350 (GlyXXSerValProXXTrp)(SEQ ID NO. 731), whereas the other group contains proteins that are unrelated except for the presence of the common 180-residue PPE domain. C-terminal extensions may range in size from 00 up to 3500 residues.

[0100] One member of the PGRS sub-family, the WHO antigen 22T (Abou-Zeid et al., 1991), a 55kD protein capable of binding fibronectin, is produced during disease and elicits a variable antibody response suggesting either that individuals mount different immune responses or that this PGRS-protein may not be produced in this form by all strains of *M. tuberculosis*. In other words, at least some PE_PGRS coding sequences

encode for proteins that are involved in the recognition of *M. tuberculosis* by the immune system of the infected host. Therefore, differences in the PGRS sequences could represent the principal source of antigenic variation in the otherwise genetically and antigenically homogeneous bacterium.

[0101] By performing the method of the invention using the *M. tuberculosis* BAC based DNA library I-1945, the inventors have discovered the occurrence of sequence differences between a given PGRS encoding ORF (ORF reference on the genomic sequence of *M. tuberculosis* Rv0746) of *M. tuberculosis* and its counterpart sequence in the genome of *M. bovis* BCG.

[0102] More precisely, the inventors have determined that one ORF contained in BAC vector N° Rv418 of the *M. tuberculosis* BCG I-1945 DNA library carries both base additions and base deletions when compared with the corresponding ORF in the genome of *M. bovis* BCG that is contained in the BAC vector N° X0175 of the *M. bovis* BCG I-2049 DNA library. The variations observed in the base sequences correspond to variations in the C-terminal part of the aminoacid sequence of the PGRS ORF translation product.

[0103] As shown in Figure 6, an amino acid stretch of 9 residues in length is present in this *M. tuberculosis* PGRS (ORf reference Rv0746) and is absent from the ORF counterpart of *M. bovis* BCG, namely the following amino acid sequence:

[0104] NH₂-GGAGGAGGSSAGGGGAGGAGGAGGWLLGD-COOH (SEQ ID NO. 732).

[0105] Furthermore, Figure 6 shows also that an amino acid stretch of 45 residues in length is absent from this *M. tuberculosis* PGRS and is present in the ORF counterpart of *M. bovis* BCG, namely following amino acid sequence:

[0106] NH₂-GAGGIGGIGGNANGGAGGNGGTGGQLWGSGGAGVEGGAAL SVGDT-COOH (SEQ ID NO. 733).

[0107] Similar observations were made with PPE ORF Rv0442, which showed a 5 codon deletion relative to a *M. bovis* amino acid sequence.

[0108] Given that the polymorphism associated with the PE-PGRS or PEE ORFS resulted in extensive antigenic variability or reduced antigen presentation, this would be of immense significance for vaccine design, for understanding protective immunity in tuberculosis and, possibly, explain the varied responses seen in different BCG vaccination programmes.

[0109] There are several striking parallels between the PGRS proteins and the Epstein-Barr virus-encoded nuclear antigens (EBNA). Both polypeptide families are

glycine-rich, contain Gly-Ala repeats that represent more than one third of the molecule, and display variation in the length of the repeat region between different isolates. The Gly-Ala repeat region of EBNA1 has been shown to function as a *cis*-acting inhibitor of antigen processing and MHC class I-restricted antigen presentation. (Levitskaya et al., 1995). The fact that MHC class I knock-out mice are extremely susceptible to *M. tuberculosis* underlines the importance of MHC class I antigen presentation in protection against tuberculosis. Therefore, it is possible that the PE/PPE protein family also play some role in inhibiting antigen presentation, allowing the bacillus to hide from the host's immune system.

[0110] As such the novel and nonobvious PGRS polynucleotide from *M. bovis* which is homolog to the *M. tuberculosis* ORF Rv0746, and which is contained in the BAC clone N° X0175 (See Table 4 for SP6 and T7 end-sequences of clone n° X0175) of the I-2049 *M. bovis* BCG BAC DNA library is part of the present invention, as it represents a starting material in order to define specific probes or primers useful for detection of antigenic variability in mycobacterial strains, possible inhibition of antigen processing as well as to differentiate *M. tuberculosis* from *M. bovis* BCG.

[0111] Thus, a further object of the invention consists in a polynucleotide comprising the sequence SEQ ID N°4.

[0112] Polynucleotides of interest have been defined by the inventors as useful detection tools in order to differentiate *M. tuberculosis* from *M. bovis* BCG. Such polynucleotides are contained in the 45 aminoacid length coding sequence that is present in *M. bovis* BCG but absent from *M. tuberculosis*. This polynucleotide has a sequence beginning (5' end) at the nucleotide at position nt 729 of the sequence SEQ ID N°4 and ending (3' end) at the nucleotide in position nt 863 of the sequence SEQ ID N°4.

[0113] Thus, part of the present invention is also a polynucleotide which is chosen among the following group of polynucleotides :

[0114] a) a polynucleotide comprising at least 8 consecutive nucleotides of the nucleotide sequence SEQ ID N°5 ;

[0115] b) a polynucleotide which sequence is fully complementary to the sequence of the polynucleotide defined in a) ;

[0116] c) a polynucleotide that hybridizes under stringent hybridization conditions with the polynucleotide defined in a) or with the polynucleotide defined in b).

[0117] The stringent hybridization conditions for the purpose of defining the above disclosed polynucleotide are defined herein before in the specification.

[0118] The invention also provides for a BAC-based *Mycobacterium tuberculosis* strain H37Rv genomic DNA library that has been deposited in the Collection Nationale de Cultures de Microorganismes on November 19, 1997 under the accession number I-1945.

[0119] A further object of the invention consists in a recombinant BAC vector which is chosen among the group consisting of the recombinant BAC vectors belonging to the BAC-based DNA library I-1945.

[0120] Generally, a recombinant BAC vector of interest may be chosen among the following set or group of BAC vectors contained in the BAC-based DNA library I-1945 :

[0121] Rv101; Rv102; Rv103; Rv104; Rv105; Rv106; Rv107; Rv108; Rv109; Rv110; Rv111; Rv112; Rv113; Rv114; Rv115; Rv116; Rv117; Rv118; Rv119; Rv120; Rv121; Rv122; Rv123; Rv124; Rv126; Rv127; Rv128; Rv129; Rv130; Rv132; Rv134; Rv135; Rv136; Rv137; Rv138; Rv139; Rv140; Rv141; Rv142; Rv143; Rv144; Rv145; Rv146; Rv147; Rv148; Rv149; Rv150; Rv151; Rv152; Rv153; Rv154; Rv155; Rv156; Rv157; Rv159; Rv160; Rv161; Rv162; Rv163; Rv164; Rv165; Rv166; Rv167; Rv169; Rv170; Rv171; Rv172; Rv173; Rv174; Rv175; Rv176; Rv177; Rv178; Rv179; Rv180; Rv181; Rv182; Rv183; Rv184; Rv185; Rv186; Rv187; Rv188; Rv189; Rv190; Rv191; Rv192; Rv193; Rv194; Rv195; Rv196; Rv197; Rv198; Rv199; Rv200; Rv201; Rv204; Rv205; Rv207; Rv209; Rv210; Rv214; Rv215; Rv217; Rv218; Rv219; Rv220; Rv221; Rv222; Rv223; Rv224; Rv225; Rv226; Rv227; Rv228; Rv229; Rv230; Rv231; Rv232; Rv233; Rv234; Rv235; Rv237; Rv240; Rv241; Rv243; Rv244; Rv245; Rv246; Rv247; Rv249; Rv250; Rv251; Rv252; Rv253; Rv254; Rv255; Rv257; Rv258; Rv259; Rv260; Rv261; Rv262; Rv263; Rv264; Rv265; Rv266; Rv267; Rv268; Rv269; Rv270; Rv271; Rv272; Rv273; Rv274; Rv275; Rv276; Rv277; Rv278; Rv279; Rv280; Rv281; Rv282; Rv283; Rv284; Rv285; Rv286; Rv287; Rv288; Rv289; Rv290; Rv291; Rv292; Rv293; Rv294; Rv295; Rv296; Rv297; Rv298; Rv299; Rv300; Rv301; Rv302; Rv303; Rv304; Rv306; Rv307; Rv308; Rv309; Rv310; Rv311; Rv312; Rv313; Rv314; Rv315; Rv316; Rv317; Rv318; Rv319; Rv320; Rv321; Rv322; Rv327; Rv328; Rv329; Rv330; Rv331; Rv333; Rv334; Rv335; Rv336; Rv337; Rv338; Rv339; Rv340; Rv341; Rv343; Rv344; Rv346; Rv347; Rv348; Rv349; Rv350; Rv351; Rv352; Rv353; Rv354; Rv355; Rv356; Rv357; Rv358; Rv359; Rv360; Rv361; Rv363; Rv364; Rv365; Rv366; Rv367; Rv368; Rv369; Rv370; Rv371; Rv373; Rv374; Rv375; Rv376; Rv377; Rv378; Rv379; Rv380; Rv381; Rv382; Rv383; Rv384; Rv385; Rv386; Rv387; Rv388;

Rv389; Rv38; Rv390; Rv391; Rv392; Rv393; Rv396; Rv39; Rv3; Rv40; Rv412; Rv413; Rv414; Rv415; Rv416; Rv417; Rv418; Rv419; Rv41; Rv42; Rv43; Rv44; Rv45; Rv46; Rv47; Rv48; Rv49; Rv4; Rv50; Rv51; Rv52; Rv53; Rv54; Rv55; Rv56; Rv57; Rv58; Rv59; Rv5; Rv60; Rv61; Rv62; Rv63; Rv64; Rv65; Rv66; Rv67; Rv68; Rv69; Rv6; Rv70; Rv71; Rv72; Rv73; Rv74; Rv75; Rv76; Rv77; Rv78; Rv79; Rv7; Rv80; Rv81; Rv82; Rv83; Rv84; Rv85; Rv86; Rv87; Rv88; Rv89; Rv8; Rv90; Rv91; Rv92; Rv94; Rv95; Rv96; Rv9.

[0122] The end sequences of the polynucleotide inserts of each of the above clones corresponding respectively to the sequences adjacent to the T7 promoter and to the Sp6 promoter on the BAC vector are shown in Table 3.

[0123] It has been shown by the inventors that the minimal overlapping set of BAC vectors of the BAC-based DNA library I-1945 contains 68 unique BAC clones and practically spans almost the whole H37Rv chromosome with the exception of a single gap of approximately 150 kb.

[0124] More specifically, a recombinant BAC vector of interest is chosen among the following set or group of BAC vectors from the BAC-based DNA library I-1945, the location of which vector DNA inserts on the chromosome of *M. tuberculosis* is shown in Figure 3 :

[0125] Rv234; Rv351; Rv166; Rv35; Rv415; Rv404; Rv209; Rv272; Rv30; Rv228; Rv233; Rb38; Rv280; Rv177; Rv48; Rv374; Rv151; Rv238; Rv156; Rv92; Rv3; Rv403; Rv322; Rv243; Rv330; Rv285; Rv233; Rv219; Rv416; Rv67; Rv222; Rv149; Rv279; Rv87; Rv273; Rv266; Rv25; Rv136; Rv414; Rv13; Rv289; Rv60; Rv104; Rv5; Rv165; Rv215; Rv329; Rv240; Rv19; Rv74; Rv411; Rv167; Rv56; Rv80; Rv164; Rv59; Rv313; Rv265; Rv308; Rv220; Rv258; Rv339; Rv121; Rv419; Rv418; Rv45; Rv217; Rv134; Rv17; Rv103; Rv21; Rv22; Rv2; Rv270; Rv267; Rv174; Rv257; Rv44; Rv71; Rv7; Rv27; Rv191; Rv230; Rv128; Rv407; Rv106; Rv39; Rv255; Rv74; Rv355; Rv268; Rv58; Rv173; Rv264; Rv417; Rv401; Rv144; Rv302; Rv81; Rv163; Rv281; Rv221; Rv420; Rv175; Rv86; Rv412; Rv73; Rv269; Rv214; Rv287; Rv42; Rv143.

[0126] The polynucleotides disclosed in Table 3 may be used as probes in order to select a given clone of the BAC DNA library I-1945 for further use.

[0127] The invention also provides for a BAC-based *Mycobacterium bovis* strain Pasteur genomic DNA library that has been deposited in the Collection Nationale de Cultures de Microorganismes on June 30, 1998 under the accession number I-2049.

[0128] A further object of the invention consists in a recombinant BAC vector which is chosen among the group consisting of the recombinant BAC vectors belonging to the BAC-based DNA library I-2049. This DNA library contains approximately 1600 clones. The average insert size is estimated to be ~80 kb.

[0129] Generally, a recombinant BAC vector of interest may be chosen among the following set or group of BAC vectors contained in the BAC-based DNA library I-2049:

[0130] X0001; X0002; X0003; X0004; X0006; X0007; X0008; X0009; X0010; X0012; X0013; X0014; X0015; X0016; X0017; X0018; X0019; X0020; X0021; X0175.

[0131] The end sequences of the polynucleotide inserts of each of the above clones corresponding respectively to the sequences adjacent to the T7 promoter and to the Sp6 promoter on the BAC vector are shown in Table 4.

[0132] The polynucleotides disclosed in Table 4 may be used as probes in order to select a given clone of the BAC DNA library I-2049 for further use.

[0133] Are also part of the invention the polynucleotide inserts that are contained in the above described BAC vectors, that are useful as primers or probes.

[0134] These polynucleotides and nucleic acid fragments may be used as primers for use in amplification reactions, or as nucleic probes.

[0135] PCR is described in the US patent N° 4,683,202. The amplified fragments may be identified by an agarose or a polyacrylamide gel electrophoresis, or by a capillary electrophoresis or alternatively by a chromatography technique (gel filtration, hydrophobic chromatography or ion exchange chromatography). The specificity of the amplification may be ensured by a molecular hybridization using, for example, one of the initial primers as nucleic probes.

[0136] Amplified nucleotide fragments are used as probes in hybridization reactions in order to detect the presence of one polynucleotide according to the present invention or in order to detect mutations in the genome of the given mycobacterium of interest, specifically a mycobacterium belonging to the *Mycobacterium tuberculosis* complex and more specifically *Mycobacterium tuberculosis* and *Mycobacterium bovis* BCG.

[0137] Are also part of the present invention the amplified nucleic fragments («amplicons») defined herein above.

[0138] These probes and amplicons may be radioactively or non-radioactively labeled, using for example enzymes or fluorescent compounds.

[0139] Other techniques related to nucleic acid amplification may also be used and are generally preferred to the PCR technique.

[0140] The Strand Displacement Amplification (SDA) technique (Walker et al., 1992) is an isothermal amplification technique based on the ability of a restriction enzyme to cleave one of the strands at his recognition site (which is under a hemiphosphorothioate form) and on the property of a DNA polymerase to initiate the synthesis of a new strand from the 3'OH end generated by the restriction enzyme and on the property of this DNA polymerase to displace the previously synthesized strand being localized downstream. The SDA method comprises two main steps:

[0141] a) The synthesis, in the presence of dCTP- α -S, of DNA molecules that are flanked by the restriction sites that may be cleaved by an appropriate enzyme.

[0142] b) The exponential amplification of these DNA molecules modified as such, by enzyme cleavage, strand displacement and copying of the displaced strands. The steps of cleavage, strand displacement and copy are repeated a sufficient number of times in order to obtain an accurate sensitivity of the assay.

[0143] The SDA technique was initially realized using the restriction endonuclease HincII but is now generally practised with an endonuclease from *Bacillus stearothermophilus* (BSOI) and a fragment of a DNA polymerase which is devoid of any 5'→3'exonuclease activity isolated from *Bacillus cladothrix* (exo- Bca) [=exo-minus-Bca]. Both enzymes are able to operate at 60°C and the system is now optimized in order to allow the use of dUTP and the decontamination by UDG. When using this technique, as described by Spargo et al. in 1996, the doubling time of the target DNA is of 26 seconds and the amplification rate is of 10^{10} after an incubation time of 15 min at 60°C.

[0144] The SDA amplification technique is more easy to perform than PCR (a single thermostated waterbath device is necessary) and is faster than the other amplification methods.

[0145] Thus, another object of the present invention consists in using the nucleic acid fragments according to the invention (primers) in a method of DNA or RNA amplification according to the SDA technique. For performing SDA, two pairs of primers are used : a pair of external primers (B1, B2) consisting of a sequence specific for the target polynucleotide of interest and a pair of internal primers (S1, S2) consisting of a fusion oligonucleotide carrying a site that is recognized by a restriction endonuclease, for example the enzyme BSOI.

[0146] The operating conditions to perform SDA with such primers are described in Spargo et al, 1996.

[0147] The polynucleotides of the invention and their above described fragments, especially the primers according to the invention, are useful as technical means for performing different target nucleic acid amplification methods such as:

[0148] - TAS (Transcription-based Amplification System), described by Kwoh et al. in 1989.

[0149] - SR (Self-Sustained Sequence Replication), described by Guatelli et al. in 1990.

[0150] - NASBA (Nucleic acid Sequence Based Amplification), described by Kievitis et al. in 1991.

[0151] - TMA (Transcription Mediated Amplification).

[0152] The polynucleotides according to the invention are also useful as technical means for performing methods for amplification or modification of a nucleic acid used as a probe, such as:

[0153] - LCR (Ligase Chain Reaction), described by Landegren et al. in 1988 and improved by Barany et al. in 1991 who employ a thermostable ligase.

[0154] - RCR (Repair Chain Reaction) described by Segev et al. in 1992.

[0155] - CPR (Cycling Probe Reaction), described by Duck et al. in 1990.

[0156] - Q-beta replicase reaction, described by Miele et al. in 1983 and improved by Chu et al. in 1986, Lizardi et al. in 1988 and by Burg et al. and Stone et al. in 1996.

[0157] When the target polynucleotide to be detected is a RNA, for example a mRNA, a reverse transcriptase enzyme will be used before the amplification reaction in order to obtain a cDNA from the RNA contained in the biological sample. The generated cDNA is subsequently used as the nucleic acid target for the primers or the probes used in an amplification process or a detection process according to the present invention.

[0158] The non-labeled polynucleotides or oligonucleotides of the invention may be directly used as probes. Nevertheless, the polynucleotides or oligonucleotides are generally labeled with a radioactive element (^{32}P , ^{35}S , ^3H , ^{125}I) or by a nonisotopic molecule (for example, biotin, acetylaminofluorene, digoxigenin, 5bromodesoxyuridin, fluorescein) in order to generate probes that are useful for numerous applications.

[0159] Examples of non-radioactive labeling, of nucleic acid -fragments are described in the french patent N° FR-7810975 or by Urdea et al. or Sanchez-Pescador et al., 1988.

[0160] In the latter case, other labeling techniques may be also used such as those described in the french patents FR-2 422 956 and 2 518 755. The hybridization step may be performed in different ways (Matthews et al., 1988). The more general method consists of immobilizing the nucleic acid that has been extracted from the biological sample onto a substrate (nitrocellulose, nylon, polystyrene) and then to incubate, in defined conditions, the target nucleic acid with the probe. Subsequently to the hybridization step, the excess amount of the specific probe is discarded and the hybrid molecules formed are detected by an appropriate method (radioactivity, fluorescence or enzyme activity measurement).

[0161] Advantageously, the probes according to the present invention may have structural characteristics such that they allow the signal amplification, such structural characteristics being, for example, branched DNA probes as those described by Urdea et al. in 1991 or in the European patent N° EP-0 225 807 (Chiron).

[0162] In another advantageous embodiment of the probes according to the present invention, the latters may be used as « capture probes », and are for this purpose immobilized on a substrate in order to capture the target nucleic acid contained in a biological sample. The captured target nucleic acid is subsequently detected with a second probe which recognizes a sequence of the target nucleic acid which is different from the sequence recognized by the capture probe.

[0163] The oligonucleotide probes according to the present invention may also be used in a detection device comprising a matrix library of probes immobilized on a substrate, the sequence of each probe of a given length being localized in a shift of one or several bases, one from the other, each probe of the matrix library thus being complementary to a distinct sequence of the target nucleic acid. Optionally, the substrate of the matrix may be a material able to act as an electron donor, the detection of the matrix positions in which an hybridization has occurred being subsequently determined by an electronic device. Such matrix libraries of probes and methods of specific detection of a target nucleic acid is described in the European patent application N° EP-0 713 016 (Affymax technologies) and also in the US patent N° US-5,202,231 (Drmanac).

[0164] Since almost the whole length of a mycobacterial chromosome is covered by a BAC-based genomic DNA libraries according to the present invention (i.e. 97% of the *M. tuberculosis* chromosome is covered by the BAC library I-1945), these DNA libraries will play an important role in a plurality of post-genomic applications, such as in mycobacterial gene expression studies where the canonical set of BACs could be used as

a matrix for hybridization studies. Probing such matrices with cDNA probes prepared from total mRNA will uncover genetic loci induced or repressed under different physiological conditions (Chuang et al., 1993; Trieselmann et al., 1992). As such, the H37Rv BAC library represents a fundamental resource for present and future genomics investigations.

[0165] The BAC vectors or the polynucleotide inserts contained therein may be directly used as probes, for example when immobilized on a substrate such as described herein before.

[0166] The BAC vectors or their polynucleotide inserts may be directly adsorbed on a nitrocellulose membrane, at predetermined locations on which one or several polynucleotides to be tested are then put to hybridize therewith.

[0167] Preferably, a collection of BAC vectors that spans the whole genome of the mycobacterium under testing will be immobilized, such as, for example, the set of 68 BAC vectors of the I-1945 DNA library that is described elsewhere in the specification and shown in Figure 3.

[0168] The immobilization and hybridization steps may be performed as described in the present Materials and Methods Section.

[0169] As another illustrative embodiment of the use of the BAC vectors of the invention as polynucleotide probes, these vectors may be useful to perform a transcriptional activity analysis of mycobacteria growing in different environmental conditions, for example under conditions in which a stress response is expected, as it is the case at an elevated temperature, for example 40°C.

[0170] In this specific embodiment of the invention, Genescreen membranes may be used to immobilize the restriction endonuclease digests (*Hind*III digests for the BAC DNA library I-1945) of the BAC vectors by transfer from a gel (Trieselmann et al., 1992).

[0171] Alternatively, the BAC vectors may be immobilized for dot blot experiments as follows. First, the DNA concentration of each BAC clone is determined by hybridization of blots of clone DNAs and of a BAC vector concentration standard with a BAC vector specific DNA probe. Hybridization is quantified by the Betascope 603 blot analyzer (Betagen Corp.), which collects beta particles directly from the blot with high efficiency. Then, 0.5 µg of each clone DNA is incubated in 0.25 M NaOH and 10 mM EDTA at 65°C for 60 min to denature the DNA and degrade residual RNA contaminants. By using a manifold filtration system (21 by 21 wells), each clone DNA is blotted onto a GeneScreen Plus nylon membrane in the alkaline solution. After neutralization, the blots

are baked at 85°C for 2 h under vacuum. Positive and negative controls are added when necessary. In order to perform this procedure, it may be referred to the article of Chuang et al. (1993).

[0172] For RNA extractions, cells grown in a suitable volume of culture medium may, for example, be immediately mixed with an equal volume of crushed ice at -70°C and spun at 4°C in a 50 ml centrifugation tube. The cell pellet is then suspended in 0.6 ml of ice-cold buffer (10 mM KCl, 5 mM MgCl, 10 mM Tris; pH 7.4) and then immediately added to 0.6 ml of hot lysis buffer (0.4 M NaCl, 40 mM EDTA, 1% beta-mercaptoethanol, 1% SDS, 20 mM Tris; pH 7.4) containing 100 µl of water saturated phenol. This mixture is incubated in a boiling water bath for 40 s. The debris are removed by centrifugation. The supernatant is extracted with phenol-chloroform five times, ethanol precipitated, and dried. The dried RNA pellet is dissolved in water before use.

[0173] Then labeled total cDNA may be prepared by the following method. The reaction mixture contains 15 µg of the previously prepared total RNA, 5 µg of pd(N₆) (random hexamers from Pharmacia Inc.), 0.5 mM dATP, 0.5 mM dGTP and 0.5 mM DTTP, 5 µM dCTP, 100 µCi of [α -³²P]dCTP (3,000 Ci/mmol), 50 mM Tris-HCl (pH 8.3), 6 mM MgCl₂, 40 mM KCl, 0.5 U of avian myeloblastosis virus reverse transcriptase (Life Science Inc.) in a total volume of 50 µl. The reaction is allowed to continue overnight at room temperature. EDTA and NaOH are then added to final concentrations of 50 mM and 0.25 M, respectively, and the mixture is incubated at 65°C for 30 min to degrade the RNA templates. The cDNA is then ready to use after neutralization by adding HCl and Tris buffer.

[0174] The hybridization step may be performed as described by Chuang et al. (1993) and briefly disclosed hereinafter. The DNA dot blot is hybridized to ³²P- labeled total cDNA in a solution containing 0.1% polyvinylpyrrolidone, 0.1% Ficoll 0.1% sodium Ppi, 0.1% bovine serum albumin, 0.5% SDS, 100 mM NaCl, and 0.1 mM sodium citrate, pH 7.2, at 65°C for 2 days and then washed with a solution containing 0.1% SDS, 100 mM NaCl, and 10 mM Na-citrate, pH 7.2. The same dot blot is used for hybridization with both control and experimental cDNAs, with an alkaline probe stripping procedure (soaked twice in 0.25M NaOH-0.75 M NaCl at room temperature, 30 min each, neutralized, and completely dried at 65°C for at least 30 min) between the two hybridizations. Quantification may be done with the Betascope 603 blot analyzer (Betagen Corp.).

[0175] As it flows from the above technical teachings, another object of the invention consists in a method for detecting the presence of mycobacteria in a biological sample comprising the steps of:

[0176] a) bringing into contact the recombinant BAC vector or a purified polynucleotide according to the invention with a biological sample ;

[0177] b) detecting the hybrid nucleic acid molecule formed between said purified polynucleotide and the nucleic acid molecules contained within the biological sample.

[0178] The invention further deals with a method for detecting the presence of mycobacteria in a biological sample comprising the steps of:

[0179] a) bringing into contact the recombinant BAC vector or a purified polynucleotide according to the invention that has been immobilized onto a substrate with a biological sample;

[0180] b) bringing into contact the hybrid nucleic acid molecule formed between said purified polynucleotide and the nucleic acid contained in the biological sample with a labeled recombinant BAC vector or a polynucleotide according to the invention, provided that said polynucleotide and polynucleotide of step a) have non-overlapping sequences.

[0181] Another object of the invention consists in a method for detecting the presence of mycobacteria in a biological sample comprising the steps of:

[0182] a) bringing into contact the nucleic acid molecules contained in the biological sample with a pair of primers according to the invention;

[0183] b) amplifying said nucleic acid molecules;

[0184] c) detecting the nucleic acid fragments that have been amplified, for example by gel electrophoresis or with a labeled polynucleotide according to the invention.

[0185] In one specific embodiment of the above detection and/or amplification methods, said methods comprise an additional step wherein before step a), the nucleic acid molecules of the biological sample have been made available to a hybridization reaction.

[0186] In another specific embodiment of the above detection methods, said methods comprise an additional step, wherein, before the detection step, the nucleic acid molecules that are not hybridized with the immobilized purified polynucleotide are removed.

[0187] Also part of the invention is a kit for detecting mycobacteria in a biological sample comprising:

[0188] a) a recombinant BAC vector or a purified polynucleotide according to the invention;

[0189] b) reagents necessary to perform a nucleic acid hybridization reaction.

[0190] The invention also pertains to a kit for detecting a mycobacteria in a biological sample comprising:

[0191] a) a recombinant BAC vector or a purified polynucleotide according to the invention that is immobilized onto a substrate;

[0192] b) reagents necessary to perform a nucleic acid hybridization reaction;

[0193] c) a purified polynucleotide according to the invention which is radioactively or non-radioactively labeled, provided that said polynucleotide and the polynucleotide of step a) have non-overlapping sequences.

[0194] Moreover, the invention provides for a kit for detecting mycobacteria in a biological sample comprising:

[0195] a) a pair of purified primers according to the invention;

[0196] b) reagents necessary to perform a nucleic acid amplification reaction;

[0197] c) optionally, a purified polynucleotide according to the invention useful as a probe.

[0198] The invention embraces also a method for detecting the presence of a genomic DNA, a cDNA or a mRNA of mycobacteria in a biological sample, comprising the steps of :

[0199] a) bringing into contact the biological sample with a plurality of BAC vectors according to the invention or purified polynucleotides according to the invention, that are immobilized on a substrate;

[0200] b) detecting the hybrid complexes formed.

[0201] The invention also provides a kit for detecting the presence of genomic DNA, cDNA or mRNA of a mycobacterium in a biological sample, comprising:

[0202] a) a substrate on which a plurality of BAC vectors according to the invention or purified polynucleotides according to the invention have been immobilized;

[0203] b) optionally, the reagents necessary to perform the hybridization reaction.

[0204] Additionally, the recombinant BAC vectors according to the invention and the polynucleotide inserts contained therein may be used for performing detection methods based on « molecular combing ». Said methods consist in methods for aligning

macromolecules, especially DNA and are applied to processes for detecting, for measuring intramolecular distance, for separating and/or for assaying a macromolecule, especially DNA in a sample.

[0205] These « molecular combing » methods are simple methods, where the triple line S/A/B (meniscus) resulting from the contact between a solvent A and the surface S and a medium B is caused to move on the said surface S, the said macromolecules (i.e. DNA) having a part, especially an end, anchored on the surface S, the other part, especially the other end, being in solution in the solvent A. These methods are particularly fully described in the PCT Application n° PCT/FR 95/00165 filed on February 11, 1994 (Bensimon et al.).

[0206] When performing the « molecular combing » method with the recombinant BAC vectors according to the inventions or their polynucleotide inserts, the latter may be immobilized (« anchored ») on a suitable substrate and aligned as described in the PCT Application n° PCT/FR 95/00165, the whole teachings of this PCT Application being hereby incorporated by reference. Then, polynucleotides to be tested, preferably under the form of radioactively or non radioactively labeled polynucleotides, that may consist of fragments of genomic DNA, cDNA etc. are brought into contact with the previously aligned polynucleotides according to the present invention and then their hybridization position on the aligned DNA molecules is determined using any suitable means including a microscope or a suitable camera device.

[0207] Thus, the present invention is also directed to a method for the detection of the presence of a polynucleotide of mycobacterial origin in a biological sample and/or for physical mapping of a polynucleotide on a genomic DNA, said method comprising:

[0208] a) aligning at least one polynucleotide contained in a recombinant BAC vector according to the invention on the surface of a substrate;

[0209] b) bringing into contact at least one polynucleotide to be tested with the substrate on which the at least one polynucleotide of step a) has been aligned;

[0210] c) detecting the presence and/or the location of the tested polynucleotide on the at least one aligned polynucleotide of step a).

[0211] The invention finally provides for a kit for performing the above method, comprising:

[0212] a) a substrate whose surface has at least one polynucleotide contained in a recombinant BAC vector according to the invention;

[0213] b) optionally, reagents necessary for labeling DNA;

[0214] c) optionally, reagents necessary for performing a hybridization reaction.

[0215] In conclusion, it may be underlined that the alliance of such BAC-based approaches such as described in the present specification to the advances in comparative genomics by the availability of an increased number of complete genomes, and the rapid increase of well-characterized gene products in the public databases, will allow the one skilled in the art an exhaustive analysis of the mycobacterial genome.

MATERIALS AND METHODS

[0216] 1. DNA-preparation. Preparation of *M tuberculosis* H37Rv DNA in agarose plugs was conducted as previously described (Canard et al., 1989; Philipp et al., 1996b). Plugs were stored in 0.2 M EDTA at 4°C and washed 3 times in 0.1% Triton X-100 buffer prior to use.

[0217] 2. BAC vector preparation. pBeloBAC11 was kindly provided by Dr. Shizuya, Department of Biology, California Institute of Technology (Pasadena, CA). The preparation followed the description of Woo et al., 1994 (Woo et al., 1994).

[0218] 3. Partial digestion with *Hind*III. Partial digestion was carried out on plugs, each containing approximately 10 µg of high molecular weight DNA, after three one hour equilibration steps in 50 ml of *Hind*III 1X digestion buffer (Boehringer Mannheim, Mannheim, Germany) plus 0.1% Triton X-100. The buffer was then removed and replaced by 1ml/plug of ice-cold *Hind*III enzyme buffer containing 20 units of *Hind*III (Boehringer). After two hours incubation on ice, the plugs were transferred to a 37°C water bath for 30 minutes. Digestions were stopped by adding 500 µl of 50 mM EDTA (pH 8.0).

[0219] 4. Size selection. The partially digested DNA was subjected to contour-clamped homogenous electric field (CHEF) electrophoresis on a 1% agarose gel using a BioRad DR III apparatus (BioRad, Hercules, CA) in IX TAE buffer at 13°C, with a ramp from 3 to 15 seconds at 6 V/cm for 16 hours. Agarose slices from 25 to 75 kb, 75 to 120 kb and 120 to 180 kb were excised from the gel and stored in TE at 4°C.

[0220] 5. Ligation and transformation. Agarose-slices containing fractions from 25 to 75 kb, 75 to 120 kb and 120 to 180 kb were melted at 65°C for 10 minutes and digested with Gelase (Epicentre Technologies, Madison, WI), using 1 unit per 100 µl gel-slice. 25-100 ng of the size-selected DNA was then ligated to 10 ng of *Hind*III digested, dephosphorylated pBeloBAC11 in a 1:10 molar ratio using 10 units of T4 DNA ligase (New England Biolabs, Beverly, MA) at 16°C for 20 hours. Ligation mixtures were heated at 65°C for 15 minutes, then drop-dialysed against TE using Millipore VS 0.025

mM membranes (Millipore, Bedford, MA). Fresh electrocompetent *E. coli* DH10B cells (Sheng et al., 1995) were harvested from 200 ml of a mid-log ($OD_{550}=0.5$) culture grown in SOB medium. Cells were washed three times in ice-cold water, and finally resuspended in ice-cold water to a cell density of 10^{11} cells/ml ($OD_{550}=150$). 1 μ l of the ligation-mix was used for electroporation of 30 μ l of electrocompetent DH10B *E. coli* using a Eurogentec Easyject Plus electroporator (Eurogentec, Seraing, Belgium), with settings of 2.5 kV, 25 μ F, and 99 Ω , in 2 mm wide electroporation cuvettes. After electroporation, cells were resuspended in 600 μ l of SOC medium, allowed to recover for 45 minutes at 37°C with gentle shaking, and then plated on LB agar containing 12.5 μ g/ml chloramphenicol (CM), 50 μ g/ml-X-gal, and 25 μ g/ml IPTG. The plates were incubated overnight and recombinants (white colonies) were picked manually to 96 well plates. Each clone was inoculated 3 times (2 X 200 μ l and 1 X 100 μ l of 2YT/12.5 μ g/ml CM per clone) and incubated overnight. One of the microtiter plates, containing 100 μ l culture per well, was maintained as a master plate at -80°C after 100 μ l of 80% glycerol were added to each well, while minipreps (Sambrook et al., 1989) were prepared from the remaining two plates to check for the presence of inserts. Clones containing inserts were then designated "Rv" clones, repicked from the master plate to a second set of plates for storage of the library at -80°C.

[0221] 6. Preparation of DNA for sizing, direct sequencing and comparative genomics. A modified Birnboim and Doly protocol (Birnboim et al., 1979) was used for extraction of plasmid DNA for sequencing purposes. Each Rv clone was inoculated into a 50 ml Falcon polypropylene tube containing 40 ml of 2YT medium with 12.5 μ g/ml of CM and grown overnight at 37°C with shaking. Cells were harvested by centrifugation and stored at -20°C. The frozen pellet was resuspended in 4 ml of Solution A (50 mM glucose, 10 mM EDTA, 25 mM Tris, pH 8.0) and 4 ml of freshly prepared solution B (0.2 M NaOH 0.2% SDS) was then added. The solution was gently mixed and kept at room temperature for 5 minutes before adding 4 ml of ice-cold solution C (3M Sodium Acetate, pH 4.7). Tubes were kept on ice for 15 min, and centrifuged at 10,000 rpm for 15 min. After isopropanol precipitation, the DNA pellet was dissolved in 600 μ l RNase solution (15 mM Tris HCl pH 8.0, 10 μ g/ml RNase A). After 30 minutes at 37°C the DNA solution was extracted with chloroform:isoamylalcohol (24:1) and precipitated from the aqueous phase using isopropanol. The DNA pellet was then rinsed with 70% ethanol, air-dried and dissolved in 30 μ l distilled water. In general, DNA prepared by this method was clean and concentrated enough to give good quality results by automatic sequencing

(at least 300 bp of sequence). For a few DNA preparations, an additional polyethylene glycol (PEG) precipitation step was necessary, which was performed as follows. The 30 µl of DNA solution were diluted to 64µl, mixed gently and precipitated using 16 µl 4M NaCl and 80 µl of 13% PEG 8000. After 30 min on ice the tubes were centrifuged at 4°C, the pellet carefully rinsed with 70% ethanol, air-dried and diluted in 20 µl of distilled water.

[0222] 7. Sizing of inserts. Insert sizes were determined by pulsed-field gel electrophoresis (PFGE) after cleavage with *DraI* (Promega). 100-200 ng of DNA was *DraI*-cleaved in 20 µl total reaction volume, following the manufacturer's recommendations, then loaded onto a 1% agarose gel and migrated using a pulse of 4 s for 15 h at 6.25 V/cm at 10°C on an LKB-Pharmacia CHEF apparatus. Mid-range and low-range PFGE markers (New England Biolabs) were used as size standards. Insert sizes were estimated after ethidium bromide staining of gels.

[0223] 8. Direct sequencing. For each sequencing reaction 7 µl BAC DNA (300-500ng), 2 µl primer (2 µM), 8 µl reaction mix of the *Taq* DyeDeoxy Terminator cycle sequencing kit (Applied Biosystems) and 3 µl distilled water were used.

[0224] After 26 cycles (96°C for 30 sec; 56°C for 15 sec; 60°C for 4 min) in a thermocycler (MJ-research Inc., Watertown, MA) DNA was precipitated using 70 µl of 70% ethanol/0.5 mM MgCl₂, centrifuged, rinsed with 70% ethanol, dried and dissolved in 2 µl of formamide/EDTA buffer. SP6 and T7 samples of 32 BAC clones were loaded onto 64 lane, 6% polyacrylamide gels and electrophoresis was performed on a Model 373A automatic DNA sequencer (Applied Biosystems) for 12 to 16 hours. The sequences of oligonucleotides used as primers are shown in Table 1.

[0225] 9. DOP-PCR. As an alternate procedure we used partially degenerate oligonucleotides in combination with vector-specific (SP6 or T7) primers to amplify insert ends of BAC clones, following a previously published protocol for P1 clones (Liu et al., 1995). The degenerate primers Deg2, Deg3, Deg4, Deg6 (Table 1) gave the best results for selected amplification of insert termini.

[0226] Table 1: Primers used for PCRs and sequencing

[0227] Vector specific Primers for DOP PCR- first amplification step:

[0228] SP6-BAC1: AGT TAG CTC ACT CAT TAG GCA (SEQ ID NO. 734)

[0229] T7-BAC1: GGA TGT GCT GCA AGG CGA TTA (SEQ ID NO. 735)

[0230] Vector specific Primers (direct sequencing, nested primer for second PCR step)

[0231] SP6 Mid: AAA CAG CTA TGA CCA TGA TTA CGC CAA (SEQ ID NO. 736)

[0232] T7-Belo2: TCC TCT AGA GTC GAC CTG CAG GCA (SEQ ID NO. 737)

[0233] Degenerate Primers:

[0234] Deg2: TCT AGA NNN NNN TCC GGC (SEQ ID NO. 738)

[0235] Deg3: TCT AGA NNN NNN GGG CCC (SEQ ID NO. 739)

[0236] Deg4: CGT TTA AAN NNN NWA GGC CG (SEQ ID NO. 740)

[0237] Deg6: GGT ACT AGT NNN NNW TCC GGC (SEQ ID NO. 741)

[0238] Primers used for the amplification of *M. bovis* DNA in polymorphic chromosomal region of Rv58:

[0239] Primer 1: ACG ACC TCA TAT TCC GAA TCC C (SEQ ID NO. 742)

[0240] Primer 2: GCA TCT GTT GAG TAC GCA CTT CC (SEQ ID NO. 743)

[0241] 10. Screening by pooled PCR. To identify particular clones in the library which could not be detected by random end-sequencing of the 400 BAC clones, PCR-screening of DNA pools was performed. Primers were designed for regions of the chromosome where no BAC coverage was apparent using cosmid-or H37Rv whole genome shotgun sequences. Primers were designed to amplify approximately 400-500 bp. Ninety-six-well plates containing 200 µl 2YT/12.5 µg/ml CM per well were inoculated with 5 µl of -80°C glycerol stock cultures each from the master plates and incubated overnight. The 96 clones of each plate were pooled by taking 20 µl of culture from each well and this procedure was repeated for 31 plates. Pooled cultures were centrifuged, the pellets were resuspended in sterile water, boiled for 5 minutes, centrifuged and the supernatants kept for PCRs. As an initial screening step, the 31 pools of a total of 2976 BACs, representing about two thirds of the library were tested for the presence of a specific clone using appropriate PCR primers. PCR was performed using 10 µl of supernatant, 5 µl of assay buffer (100 mM b-mercaptoethanol, 600 mM Tris HCl (pH 8.8), 20 mM MgCl₂, 170 mM (NH₄)₂SO₄), 5 µl of Dimethylsulfoxide (DMSO), 5 µl of dNTPs (20 mM), 5 µl of water, 10 µl primer (2 µM), 10 µl inverse primer (2 µM) and 0.2 units of *Taq* DNA polymerase (Boehringer). 32 cycles of PCR (95°C for 30 s, 55°C for 1 min 30 s, 72°C for 2 min) were performed after an initial denaturation at 95°C for 1 min. An extension step at 72°C for 5 min finished the PCR. If a pool of 96 clones yielded an appropriate PCR product (Fig. 1A), subpools were made to identify the specific clone. Subpools representative for lane A of a 96 well plate were made by

pooling clones 1 to 12 from lane A into a separate tube. Subpools for lanes B to H were made in the same way. In addition, subpools of each of the 12 rows (containing 8 clones each) were made, so that for one 96 well plate, 20 subpools were obtained. PCR with these 20 subpools identified the specific clone (Fig. 1B, lower gel portion). If more than one specific clone was present among the 96 clones of one plate (Fig. 1B, upper gel portion), additional PCR reactions had to be performed with the possible candidates (data not shown).

[0242] 11. Genomic comparisons. DNA from the BAC clone Rv58 was digested with the restriction endonucleases *Eco*R1 and *Pvu*II, and resolved by agarose gel electrophoresis at low voltage overnight (1.5 V/cm). DNA was transferred via the method of Southern to nitrocellulose membranes (Hybond C extra, Amersham) following standard protocols (Sambrook et al., 1989), then fixed to the membranes at 80°C for 2 hours. The blot was hybridized with ³²P labelled total genomic DNA from *M. tuberculosis* H37Rv, *M. bovis* type strain (ATCC 19210) or *M. bovis* BCG Pasteur. Hybridization was performed at 37°C overnight in 50% formamide hybridization buffer as previously described (Philipp et al., 1996b). Results were interpreted from the autoradiograms.

[0243] 12. Computer analysis. Sequence data from the automated sequencer ABI373A were transferred as binary data to a Digital Alpha 200 station or Sun SparcII station and analysed using TED, a sequence analysis program from the Staden software package (Dear et al., 1991). Proof-read sequences were compared using the BLAST programs (Altschul et al., 1990) to the *M. tuberculosis* H37Rv sequence databases of the Sanger Centre, containing the collected cosmid sequences (TB.dbs) and whole-genome shotgun reads (TB_shotgun_all.dbs) (<http://www.sanger.ac.uk/>). In addition, local databases containing 1520 cosmid end-sequences and the accumulating BAC end-sequences were used to determine the exact location of end-sequenced BACs on the physical and genetic map. MycDB (Bergh et al., 1994) and public databases (EMBL, Genbank) were also used to compare new sequences, but to a lesser extent. The organization of the open reading frames (ORFs) in the polymorphic region of clone Rv58 was determined using the DIANA software established at the Sanger Centre.

EXAMPLES

[0244] Example 1 : Construction of a pBeloBAC11 library of *M. tuberculosis* H37Rv.

[0245] Partial *Hind*III fragments of H37Rv DNA in the size range of 25 to 180 kb were ligated into pBeloBAC11 and electroporated into strain *E. coli* DH10B. While cloning of fractions I (25 to 75 kb) and II (75 to 120 kb) gave approximately 4×10^4 transformants (white colonies), cloning of fraction III (120 to 180 kb) repeatedly resulted in empty clones. Parallel cloning experiments using partial *Hind*III digests of human DNA resulted in stable inserts for all three fractions (data not shown), suggesting that the maximum size of large inserts in BAC clones is strongly dependent on the source of the DNA. Analysis of the clones for the presence of inserts revealed that 70% of the clones had an insert of the appropriate size while the remaining 30% of white colonies represented empty or *lacZ'*-mutated clones. Size determination of randomly selected, *Dra*Icleaved BACs via PFGE showed that the insert sizes ranged for the majority of the clones between 40 kb and 100 kb with an average size of 70 kb. Clones with inserts of appropriate size were designated with "Rv" numbers, recultured and stored at -80°C for further use.

[0246] Example 2 : Direct DNA sequence analysis of BACs.

[0247] To characterize the BAC clones, they were systematically subjected to insert termini sequencing. Two approaches, direct sequencing of BAC DNA and PCR with degenerate oligonucleotide primers (DOP), adapted to the high G+C content of mycobacterial DNA, were used. In a first screening phase, 50 BAC clones designated Rv1 to Rv50 were analysed using both methods in parallel. Except for two clones, where the sequences diverged significantly, the sequences obtained by the two methods only differed in length. Sequences obtained directly were on average about 350 bp long and for 95% of the clones both the SP6 and T7 end-sequences were obtained at the first attempt. Sequences obtained by DOP-PCR were mostly shorter than 300 bp. For 40% of the BACs we obtained only very short amplicons of 50 to 100 base pairs from one end. In two cases the sequence obtained with the DOP-PCR differed from the sequences obtained by direct sequencing, and in these cases *E. coli* or vector sequences were amplified (data not shown). Taking the advantages and disadvantages of both methods into account, we decided to use direct termini sequencing for the systematic determination of the SP6 and T7 end-sequences.

[0248] Example 3 : Representativity of the library.

[0249] After having determined the end-sequences of 400 BACs a certain redundancy was seen. The majority of clones were represented at least 3 to 4 times. Maximum redundancy was seen in the vicinity of the unique *rrn* operon, as 2.5% of the

clones carried identical fragments that bridge the cosmids Y50 and Y130 (Fig. 3, approximate position at 1440 kb). The majority of clones with identical inserts appeared as two variants, corresponding to both possible orientations of the *Hind*III fragment in pBeloBACII. This suggests that the redundancy was not the result of amplification during library construction, but due to the limited number of possible combinations of partial *Hind*III fragments in the given size-range of 25 to 120 kb. To detect rare BAC clones, a pooled PCR protocol was used. Primers were designed on the basis of the existing cosmid sequences and used to screen 31 pools of 96 BAC clones. When positive PCR products of the correct size were obtained, smaller subpools (of 8 or 12 clones each) of the corresponding pool were subsequently used to identify the corresponding clone (Figs. 1A and 1B). With this approach 20 additional BACs (Rv401-Rv420) were found for the regions where no BACs were found with the initial systematic sequencing approach. The end-sequences of these BACs (Rv401-420) were determined by direct sequencing, which confirmed the predicted location of the clones on the chromosome. A 97% coverage of the genome of H37Rv with BAC clones was obtained. Only one region of ~ 150 kb was apparently not represented in the BAC library as screening of all pools with several sets of specific primers did not reveal the corresponding clone. This was probably due to the fact that *Hind*III fragments of mycobacterial DNA larger than 110 kb are very difficult to establish in *E. coli* and that a *Hind*III fragment of ~ 120 kb is present in this region of the chromosome (data not shown).

[0250] Example 4: Establishing a BAC map.

[0251] Using all end-sequence and shotgun-sequence data from the H37Rv genome sequencing project, most of the BAC clones could then be localized by sequence comparison on the integrated map of the chromosome of *M. tuberculosis* strain H37Rv (Philipp et al., 1996b) and an ordered physical map of the BAC-clones was established. PCR with primers from the termini sequences of selected BACs were used for chromosomal walking and confirmation of overlapping BACs (data not shown). The correct order of BACs on the map was also confirmed more recently, using 40,000 whole genome shotgun reads established at the Sanger Centre. In addition, pulsed-field gel electrophoresis of *Dra*I digests of selected BACs was performed (Fig. 2) in order to see if the approximate fragment size and the presence or absence of *Dra*I cleavage sites in the insert were consistent with the location of the BACs on the physical map (Fig. 3). Comparison of the sequence-based BAC-map with the physical and genetic map, established by PFGE and hybridization experiments (Philipp et al., 1996b), showed that

the two maps were in good agreement. The positions of 8 genetic markers previously shown on the physical and genetic map were directly confirmed by BAC-end-sequence data (Table 2, Fig. 3). The position of 43 from 47 Y-clones (91%) shown on the physical and genetic map, which were later shotgun sequenced, was confirmed by the BAC end-sequences and shotgun sequence data. Four clones (Y63, Y180, Y251, and Y253) were located to different positions than previously thought and this was found to be due to book keeping errors or to chimeric inserts. Their present approximate location relative to the *oriC* is shown in Figure 3: Y63 at 380 kb, Y63A at 2300 kb, Y180 at 2160 kb, Y251 at 100 kb, and Y253 at 2700 kb. A total of 48 BACs, covering regions of the chromosome, not represented by cosmids were then shotgun sequenced (Cole et al., 1997), and these are squared in Fig. 3. No chimeric BACs were found, which is consistent with the observations of other research groups for other BAC libraries (Cai et al., 1995; Zimmer et al., 1997). The absence of chimeric BACs was of particular importance for the correct assembly of the *M. tuberculosis* H37Rv sequence. The exact position of the BAC termini sequences on the chromosome will be available via the world wide web (<http://www.pasteur.fr/MycDB>).

[0252] Table 2 : Identities of genetic markers previously shown on the integrated and genetic map of H37Rv. (Phlipp et al., 1996b) which showed perfect sequence homology with BAC end sequences.

Locus	BAC end sequence	Description of genetic marker	Organism	GenBank Accession n°
<i>apa</i>	Rv163SP6	Secreted alanine-proline-rich antigen	<i>M. tuberculosis</i> <i>M. leprae</i>	X80268 M95576
<i>dnaJ, dnaK</i>	Rv164T7	DnaJ hsp	<i>M. tuberculosis</i>	M27016
<i>fop-A</i>	Rv136T7	Fibronectin binding protein	<i>M. tuberculosis</i> <i>M. leprae</i>	L11920 S82044
<i>polA</i>	Rv401T7	DNA polymerase I	<i>M. tuberculosis</i>	Z48057
<i>ponA</i>	Rv273T7	Penicillin binding protein	<i>M. tuberculosis</i>	X58485
<i>pstC</i>	Rv103T7	Putative phosphate transport receptor	<i>M. tuberculosis</i>	M69187
<i>recA</i>	Rv415SP6	Homologous recombination		
<i>wag9</i>	Rv35SP6	35-kDa antigen		

[0253] Example 5 : Repetitive end-sequences.

[0254] Repetitive sequences can seriously confound mapping and sequence assembly. In the case of the BAC end-sequences, no particular problems with repetitive sequences were observed. Although nine clones with one end in an *IS1081* (Collins et al., 1991) sequence were identified, it was possible to correctly locate their position on the map using the sequence of the second terminus. Moreover, these BACs were used to determine the exact locations of *IS1081* sequences on the map. Five copies of this insertion sequence, which harbors a *HindIII* cleavage site, were mapped on the previous physical and genetic map. In contrast, BAC end-sequence data revealed an additional copy of *IS1081* on the *M. tuberculosis* H37Rv chromosome. The additional copy was identified by six clones (Rv27, Rv118, Rv142, Rv160, Rv190, Rv371) which harbored an identical fragment linking Y50 to I364 (Fig. 3, at ~ 1380 kb). This copy of *IS1081* was not found by previous hybridization experiments probably because it is located near another copy of *IS1081*, localized on the same *DraI* fragment Z7 and *AsnI* fragment U (Fig. 3, at ~ 1140 kb). Furthermore, the position of a copy of *IS1081* previously shown in *DraI* fragment Y1 (Fig. 3, at ~1840 kb) had to be changed to the region of Y349 (Fig. 3, at ~ 3340 kb) according to the end-sequences of BAC Rv223. The positions of the four other *IS1081* copies were confirmed by the sequence data and therefore remained unchanged. In total 6 copies of *IS1081* were identified in the H37Rv genome in agreement with the findings of others (Collins et al., 1991).

[0255] In addition, a sequence of 1165 bp in length containing a *HindIII* site was found in two copies in the genome of H37Rv in different regions. The end-sequences of BAC clones Rv48 and Rv374, covering cosmid Y164, as well as Rv419 and Rv45, that cover cosmid Y92, had perfect identity with the corresponding parts of this 1165 bp sequence (Fig. 3, at ~ 3480 kb and ~ 900 kb). Analysis of the sequence did not reveal any homology with insertion sequences or other repetitive elements. However, as each of the two locations showed appropriate BAC coverage, chimerism of the sequenced cosmids Y164 and Y92 can be ruled out as the probable cause.

[0256] Example 6 : Using BAC clones in comparative genomics.

[0257] The minimal overlapping set of BAC clones represents a powerful tool for comparative genomics. For example, with each BAC clone containing on average an insert of 70 kb, it should be possible to cover a 1Mb section of the chromosome with 15 BAC clones. Restriction digests of overlapping clones can then be blotted to membranes, and probed with radiolabelled total genomic DNA from, for example, *M. bovis* BCG Pasteur. Restriction fragments that fail to hybridize with the *M. bovis* BCG Pasteur DNA

must be absent from its genome, hence identifying polymorphic regions between *M. bovis* BCG Pasteur and *M. tuberculosis* H37Rv. The results of such an analysis with clone Rv58 (Fig. 3, at ~ 1680 kb) are shown here. This clone covers a previously described polymorphic genomic region between *M. tuberculosis* and *M. bovis* BCG strains (Philipp et al., 1996a). *Eco*RI and *Pvu*II digests from clone Rv58, fixed on nitrocellulose membranes, were hybridized with ³²P-labelled total genomic DNA from *M. tuberculosis* H37Rv, *M. bovis* (ATCC 19120), and *M. bovis* BCG Pasteur. Figures 4A and 4B present the results of this analysis, where it is clear that several restriction fragments from clone Rv58 failed to hybridize with genomic DNA from either *M. bovis* or *M. bovis* BCG Pasteur. On the basis of the various missing restriction fragments, a restriction map of the polymorphic region was established and compared to the H37Rv sequence data. The localization of the polymorphism could therefore be estimated, and appropriate oligonucleotide primers (Table 1) were selected for the amplification and sequencing of the corresponding region in *M. bovis*. The alignment of *M. bovis* and *M. tuberculosis* H37Rv sequences showed that 12,732 bp were absent from the chromosomal region of the *M. bovis* type strain and *M. bovis* BCG Pasteur strain. The G+C content of the polymorphic region is 62.3 mol%, which is the same as the average genome G+C content of the *M. tuberculosis* genome, hence indicating that this region is not a prophage or other such insertion. Subsequent PCR studies revealed that this segment was also absent from the Danish, Russian, and Glaxo substrains of *M. bovis* BCG, suggesting that this polymorphism can be used to distinguish *M. bovis* from *M. tuberculosis*. Analysis of this sequence showed that 11 putative open reading frames (ORFs) are present in *M. tuberculosis*, corresponding to ORFs MTCY277.28 to MTCY277.38 / accession number Z79701 -EMBL Nucleotide Sequence Data Library (Fig. 5). FASTA searches against the protein and nucleic acid databases revealed that the genes of this region may be involved in polysaccharide biosynthesis. Among these putative genes, the highest score was seen with ORF 6 (MTCY277.33), whose putative product shows a 51.9% identity with GDP-D-Mannose dehydratase from *Pseudomonas aeruginosa* (accession number U18320 - EMBL Nucleotide Sequence Data Library) in a 320 amino acid overlap. The novel *M. bovis* sequence of the polymorphic region was deposited under accession number AJ003103 in the EMBL Nucleotide Sequence Data Library.

[0258] As it appears from the teachings of the specification, the invention is not limited in scope to one or several of the above detailed embodiments; the present invention also embraces all the alternatives that can be performed by one skilled in the same technical field, without deviating from the subject or from the scope of the instant invention.

Clone Rv7

:::Rv7SP6.seq:::

ATACTCAAGCTTATCTAGGCGCCAGCTTGATTGGTCTGGTTGCATTGGCCAGCTGCGCGAGCCTGGCTCACTTCAACT
ACAACAACCGCAAACAATTGCCGCTTCGGATCCGAGTTTCGGTTGGGTACGCGGCAATGGANACCATTTCTCGGTGA
ATCAGACTATTCTGAGTACTTGATCATCCACTCTGCACACGACCTGCGAACCCCGCGCGCCTTGCCGACCTGGAGC
AGCTGGCGCAACGTGTGAGCCANATCCCAGGCGTTGCCATGGTTTCGGGTGTGACCCGGCCAAACGGGGAAACCTTG
AACAGGCCCGGGCGACATACCAAGCCGGCCAAGTTGGCAACCGGCTGGGCGCGCGCTCGCGAATGATCGATGAGCGCA
CCGGCGACCTGAATCGGCTGGCATCGGGTGCCAACTGTTGGCCGACAATCTCGGTGACTTCGCGGTCAAGTCAGCCG
GGCCGTTGCGGGTGTCCGAGCCTTGTCAGCCCTCGCTTACTCCA (SEQ ID NO. 656)

:::Rv7T7.seq:::

CAGGCATGCAAGCTTTTGGAGCGTCGCGCGGGGCGAGCTTCGCCGGCAATTCTACTAGCGAGAAGTCTGGCCCGATACG
GATCTGACCGAAGTCGCTGCGGTGCAGCCACCTCATTGGCGATGGCGCCGACGATGGCGCCTGGACCGATCTTGTG
CCGCTTGCCGACGCGGACGCGGTAGTGGTCAAGTCCGGTCTACGCTTGGGCCTTTGCGGACGGTCCCAGCGTGGTC
GCGGTTGCGCCGCGAAAGCGGGTGGGTGCGGTGATCGAAGTCCGGTCTACGCTTGGGCCTTTGCGGACGGTCCCAGCGTGGTC
CGGGGATTGAGCCATCGGGACATCATGCTCGCTTACACTCTCGACCAAGTCGGCGGAACAGCTCGATTCCCGGAACG
CCCACGCGATGGTG (SEQ ID NO. 657)

Clone Rv80

:::Rv80SP6.seq:::

AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGTAAGAAAAGATCGGTGA
GCGCATCGATTGCTCCGCCGGGTTTGGCGCTGCGGCGGGGAGCTGCCGTGACCGTCTATTGGGTGATCAGACTG
GGGCTAGTTCGGTTCGGGTGGGGTGGGTGATCGAAGATCGCGGTGGCCGGCAGCGTTACTGCGGTGACAGCTGTTAAGCGGT
TACGTATCTCCACGGCACTCAAGGAATTAATCCCGAATCGGCAAACGCCTGGCCAGCGTCNAGTCCGGCAGCGCCGT
CNCGCCCCAGCACCGCTGCGGCATGCTCACATACCACCTCGATCGCTGCGGCGANTTGCTCGTCNGCCGACCGACCGG
CCANCCGGGCGGCAAACCCNGAAGACCCAAGAAATCATCACCACCATCGCTAGC (SEQ ID NO. 658)

:::Rv80T7.seq:::

CCTTCTTGACACCCACCTCGCCATCGACCTTGAGCACTCCGTCTGATGTTGGTGAACATGTGACCGGCGATCGGGCGGG
TGAACGCGTACTGGGTGTGCGGTGTGACGTTTCATCTTACCACGCCGTAGCGCAGCGCCTCTCGATCTCCGACTTAA
GCGAACCCGAGCCGCGTGAACACGAAATCNAACGGCTTGGCGTCNGCCGGCAGTCCGAGCTTGGCCGCGCCACCT
GTTGCCCTTGCGCAAGGATGTGNGGGCGAANCTTGACGTTGCCGGGCTTGANACGCCATGCACGTTGCCGAACGTCN
CGGCCAGCANGTATTTGCCGTGCTCACCGCGCGCCANCGCCTCGATGGTCTTCTCGAAGTCTCCGGGCTGGTGTACA
GCTTCTCGTTGATCTCGTTCGCCACGCGCTCCTCTCGCCGCGGACG (SEQ ID NO. 659)

Clone Rv81

:::Rv81SP6.seq:::

AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGGAAGGAGATCCCCGGG
AACCTGGTGGCAACCCCGCCATTGGGGTTGTTGGGATTGCCGATCAGCGTGAANGAAAGCTCGTCTGGAGACAGCGGG
TCGGCCGAAGCCGAAGATTGGCCATCACTAGTGACGANATCGTGGCGCTCTGCGAGTANCCNAAGACAGTGAAGT
TTNCCGGCGGCAATTTGCTGCCGAATCGCACTTTGAGAAATGACNGCACCTGCGCCACCGANGAATCNAAAGTGAGG
TTCTTGATCAGACACCGGGTNGAGCCCTTGGGGCGTGAAGANCGCCTGCGCNATAACACCCGGGACGCTGCCACTC
ATGTNACGCGGTTGCGGANCTCNACATATCT (SEQ ID NO. 660)

:::Rv81T7.seq:::

TCCTGGTGATCGANGGCGCGGTTCCGGCCGAAATCCGGTTCGGGTTCCGGTTCGCGGTTCCAACCTTGANCGCGGTCC
GCAGCTGATTACCGTGGCAACGCGGCAACTGCGCATAATGCGCATCCGAACCCCTCACCCGCGCGCCGCGATCA
CCCCAACCTGATCCAACGACAACCGCCCTCCCGCATACCCCGGGCGCAGCGCGGAACTCCGGCAACGCGCGGCCA
CCGTGGCGATCGTGTGGGCGTTGCTGACGAACANCCCATCTTCCAGGCCACCAACCCCGCCACCGACCGCGCCCCG
TCACACCCCAACCCGTGCGGATCCAGCTCAGCCACGATCTCCACAATGCGCCCATCAATCGCATTCGCTGAACGG
GCAACTCCGCCAATCCTCCAA (SEQ ID NO. 661)

Clone Rv82

:::Rv82SP6.seq:::

AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGATCTGGTACCCATCCGTGATA
CATTGAGGCTGTTCCCTGGGGTTCGTTACCTTCCACGAGCAAAACACGTAGCCCTTCAGAGCCAGATCCTGAGCAAG
ATGAACAGAACTGAGGTTTTGTAAACGCCACCTTTATGGGCGAGCAACCCCGATCACCGGTGGAAATACGTCTTCAGC
ACGTGCAATCGCGTACCAACACATCAGCATATGATTAATTTGTTCAATTGTATAACCAACAGGTTGCTCAACCCG

TCCTCGAATTTCCATATCCGGGTGCGGTAGTCGCCCTGCTTTCTCGGCATCTCTGATAGCCTGAGAAGAAACCCCAAC
TAAATCCGCTGCTTCACCTATTCTCCAGCGCCGGGTATTTTCTCGCTTCCGGGCTGTCACTATAAAGTGTGCAA

(SEQ ID NO. 662)

Clone Rv83

.....Rv83SP6.seq:.....

AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTANCGCCACCTCCCGGGCG
GAACTCCACGGCGTGGATNAAGGTACCGGCCGGGATGTTGCCAATGGCAGGTTGTTGCCCGGCTTGANGTCCGCGTT
AGCGCCGGATTCCACCACATCCCCTTGGCAAANTCCGTTGGGTNCNATGATGTNNCGCTTCTCCCNCTCNANATAATG
GANCAACGCNATCCGTGCGGTACGGTTCGGGTCTACTCCATGTNCGCGACCTTGGCGTTGANACCATCTTTGTCATT
GCGGCGAAAGTCNATCATCCGCTNAGCNCNATGANCGCCGCTTTGTGCCGGGTGGTAATCCGGCCATGCGCNTT
GCGTCCACCGCAACGTGCAACGGGGGCNCAACGANTTCTCNGGGTTGAACCGGTNATCT

(SEQ ID NO. 663)

.....Rv83T7.seq:.....

TGTGTGTGGTGGTAACCCATCTGAGCAGTGTGCCAAACGGGGCAGCCAGCTCCCAATTGACGTGAGCCCGCTCACTT
GCTGGGTAAGCGTCG

(SEQ ID NO. 664)

Clone Rv84

.....Rv84SP6.seq:.....

AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATANAATACTCAAGCTTGC GG GTNATNGCCTTGGT
CAACGGCACCGTGATCGGATCNGGGTCTACCGCACACATNGACTGGAGCTTCGGCGAANTCATCGCCTATGCCTCGCG
GGGGGTGACGCTGANCCNGGTGACNTGTTGNGCTCNGGCACGGTGCCACCTGCACGCTCNTCNAACACCTCANGCC
ACCGGAATCATTTCCNNGGCTGGCTGCACGANAGCGANNTTGTNCNCCCTCCAAGTCTAAAGGCTGGGCGANANAAGCAN
AACGTCCCGACNAACGGCACTCCTTTTCCNTTGTCTTTC

(SEQ ID NO. 665)

.....Rv84T7.seq:.....

GAAATCATTGATGGTTTGTAGTCACCAGGCGGATCAAGCCTTCGCCGAGCCAAATTCCAATCAAGAGGCCCAAGCCCGT
ACCAATCAGCCCCGGCAACGAGGGATTCCGTATTATCAGCCAAAATAACTGCTCTCGGGTTACACCCAAACAGCGCAA
TATGGCGAAAAACGGTCCGCGTTGCACGACATTAAATGTACCGGTATTGTAGATTAAAAAGATACCCACCAACAANGC
AATCAAATGAGAGCGGTTAAATTGACCGTAAAAGCGTCCGTATCTGTTTGACNGTGTCCGCTTGGGTATCCGACGT
TTCCATACGCACACCGGCCGGCAGTCTTTGTTGGATGCGTNTTGAATGGCCTCATCTTTGATGATCAAATCGATGTN
GCTCAGTCTTCCGGGCATATGGAACAACCTTGGGCCGTGGAAATATCAGCAATGATA

(SEQ ID NO. 666)

Clone Rv85

.....Rv85SP6.seq:.....

CTTTCGCCCAGGCCGCGCGGATGTCCTCATCGCTTACGAACATCATCCGAGCTTGACGCTGTCCCGAACAGATCC
GCGCTGCCGGCCGCGCGCCACACCGTTGCCGCCGATCTGGCCCATCCCGAGGTGACCGCGCAGCTGGCTGGTCAAG
CCGTCCGAGCTTTCGGGAAGCTCGACATCGTCGTAACAACGTTGGCGGCACCATGCCCAACAGCTGCTAAGCACCT
GACCAANGACCTCGCGGACGCTTTCGCTTCAACGTGGGCACCGCCACGCGCTGACCGTCCGCGCGGTGCGCTTGA
TGCTGGAACACTCCGGCGGCGGCGAGCGTGATCAACATCAGCTCCACCATGGGCGGCTGGCGGCGCGGGTTTC

(SEQ ID NO. 667)

.....Rv85T7.seq:.....

TGTGGGCTCCGATCCGGCGCGCATGGCATCGACGGCGACGCCGATCGATGACGGCCAGGCTTACGAGCTTGAGGGTGT
GAAGTTGTGGACCACCAACGGTGTGGTAGCGGACCTGCTAGTGGTTATGGCGCGGGTACCGCGCAGTGAAGGGCNC
AGGGGGAATCANCGCCTTTGTGTCGAGGCTGATTGCGCCGGGATCACCGTGGAGCGGCGCAACAAGTTTCATGGGACT
GCGTGGCATCGAAAACGGCGTGACCCGGCTTCNTCGCGTCAGGGTGCCCAAAGACAACCTTGATCGCANOGGAAGCGACG
GTCTGAAGATCGCGCTGACCACACTCAACGCCGACGGCTGTCCCTACCGCGCATCAACCGGAGT

(SEQ ID NO. 668)

Clone Rv86

.....Rv86SP6.seq:.....

GAGCTGGCCGAGCTGGACCGGTTACCGCGGAACACTACCGTTCTCGCTCGACGACTTTACGACGCGGGCTTGACGCGCG
CTGGAACGCGGCCACGGTGTGCTGGTGTGCGCGCCGACCGGCGCTGGCAAGACAGTGGTGGCGAGTTGCGCGTGCAC
CTGGCGCTGGCGGCCGCGCAGTAAATGTTTCTACACCACGCCGCTGAAAGCCCTGAGCAACCAAAAGCACACCGATCTC
ACAGCAGCTACGCGCGTGACCAAGATCTGGCTGCTGACCGGTGACCTGTGCTCAACGGCAACCGCGGTGGTGGTGA
TGACCACCGAAATGCTGCGCAACATGCTCTAC

(SEQ ID NO. 669)

.....Rv86T7.seq:.....
GATCTCTGGATCGGCGGGGCTCTCCGGGCGGCGCTCGGCGACCTCAGCGGGCCGCGCCTTCCGGCCGAACCATTCCT
AGCCATAGATGACCGCACCTCGATGCACGGTTTGGCGGCAACGCGGCAAGCGCTCNGTCGGGCCCAGCCGCGGCAATG
CGGGTACCCGGGAGCGCGGTCNGTANACCANCGCTGGACTGCGTCGCGCGGTGCGTCNACNTCAAAGTCCCCGGCGT
CCCATATCGCGTATGACGCGGGCGCGCCCGGCACCANGGGTGCCGATCCGGCCGTCTCGAACACCACCGGCCCCGCCAG
CCGCCGCGGGTCCGGCAGCNAACCCGCCCGCGCGGATACCCGCTGCCGCGTGCGTGATTGACCGCCGCGCGCACGCT
GGCCANGGATCAAAGCCCGTG (SEQ ID NO. 670)

Clone Rv87

.....Rv87SP6.seq:.....
GGACGCGTAGCCCGCCAGGCCGTCAGGGTGCCCTTCCAGTCCACGCCGCTGTGGTCCGGCAACCGCTTATCTTCAAT
CGAGACGATCGCCAGCTTCATCGTGTGGCGATCTTGTCCGAGGGCACCTCGAACCGGCGTGCGAGTNCAGCCACGC
GATCGTGTGGCCCTTCGCGTCGACCATCGTCGATACCCGAGGCACCTGCCCTCGAGCAGCTGGGCCGAGCCGTTGGC
AACGACCTCAGANGCACGATTGGACATCAGCCCTAGCCCGCTGCGAACGGGAACGTGAGCGCAGTGGCGACGACACT
GGCCAACAGACAGCACCCAGCCAGCTTCAGAACGGTGATCGCGGCCGGGAAGCGCTCGGGCATGCGTNTACAGTAGC
GACCTCCTGTCACTCCACGTGCCGCTCGGTCCAATAGAATCTTCCGCGGGCGGGTGAATCTCTGCNGGATCGGGGCN
GGCGC (SEQ ID NO. 671)

.....Rv87T7.seq:.....
GCTCGTTGCCGGCGGCGATCTCGTCGAGCTCGTCTTCCATCGCCGCGGTGAAGTCGTAGTCGACGAGCCGACCGAAAT
GCTGCTCGAGCAGACCGGTTACCGCGAACGCCACCCATGACGGCACCACTGCACTGCCCTTCTGTGACGNTGCCGC
GATCCTGGATGGTCTTGATGATCGACGANTAGGTGACGGGCGGCGATGCCAGCTCCTCGAGCGCTTTGACGAGCG
ACGCCTCNGTGTNNCGGGCCGGCGGGTGGTGGCATGGCCGTCTGGGGTCAACTCGACNATGTCCAACCGTTGACCCG
GGGTGAGATGGGGCAGTCGCCGCTCGGCATCGTCAGCCTCGCCGC (SEQ ID NO. 672)

Clone Rv88

.....Rv88SP6.seq:.....
GTCTTTTCGATGGCTGCTTCTTCGGCGCTGACGCTGGCGATCTATCACCCCCAGCAGTTTCGTCTACGCGGGAGCGATGT
CGGGCCTGTTGGACCCCTCCAGGCGATGGGTCCCACCCTGATCGGCCTGGCGATGGGTGACGCTGGCGGCTACAAGG
CCTCCGACATGTGGGGCCCGAAGGAGGACCCGGCGTGGCAGCGCAACGACCCGCTGTTGAACGTCNGGAANCTGATCG
CCAACNACACCCNCGTCTGGGTGTACTGCGGCAACNGCAAGCCGTGGATCTGGGTGGCAACAACCTGCCGGCCAAGT
TCCTCGAGGGCTTCGTGCGGACCATCAACATCAAGTTCCAAGACGCTACAACGCCNGTGGCGGCCACAACCGCGTGT
TCGACTTCCCGG (SEQ ID NO. 673)

.....Rv88T7.seq:.....
GCCAGGTCGAGGTCCCATGCGCGTGGGCCATTGATGCTGATCGCCAGGACGTCAAANATTTGGTCCGGCGTCAGCTGG
GCGAAAAACGTGGGCCCCAGGACTTGCCCGGAGCTGCCCGGGTCCCGTCGCGCAGCTCGGCGGCCCCGGTCAGAAAN
AAATTGCGCCAGGTGCGCACACTCCGCGCCGTANGCCAGCTGCTCCAGGGTGTGGGCATAGAGCCCGCGGGCCGACGG
TGCTCGCTGTGCGGCAACACCGCATGGTTCGAGAAGCGTTGCCGCCAACGGAAATCACCTGCGTCNAANGCTTCGCGG
GCCAACTCCAGCACTCGGTCGATG (SEQ ID NO. 674)

Clone Rv89

.....Rv89SP6.seq:.....
NAAACGTTCCGGCTTNGGTGCCGGGCGCTTATTTGCGTCTCTGGGATCACNCTCAGTCGCCGGGCGGCTGCCGTTGGGC
TATNANTTGCACCGANCCGAAAAATCCGCACNANAACGTCNAGTAGCGGCCTGCAGAAATGCATCCTCGGCGAANCNG
ACTACCGGTGGACANCNACAAGCGCCGCGGAACAACGCACTGGCCCCGAGGGATNGGCGTCTATCGGCCCCCGCCGTCG
AACTNGGAACAGACNGTGGGTTCTACCGTGATCTGGTGGGAATGCTCNACCANACCTTCCCNANNGCTACGGAACNA
CGGCGCGATATTNCGCCNTCCCANCTCGAGCCTGACNCTNGATATCGTCGANNCTCACCATCNCGATCNGCTGTGCCG
GTNTTGCTCGGACTN (SEQ ID NO. 675)

.....Rv89T7.seq:.....
CGAACGACGAACNCCNCAAGCCATGGTGGTTGGCGCGCTCAAAAGGTCCGCGGTGCCCACTACTGGAAATCGCCTTG
AGCGTCNCTCGACCNCCGCTCGAGTTGGGTGNTAACGAAATACCTGATGCCGATCANGTCNACGTCTCCGTGCGNNC
AACGTGACGCGGCGACCACTCTACNANGTCTCGGTNCCGCCNCGGCCAGNGCACCACCACTGACNAATCCNTGCGCC
NTCGGGCCNAGCANTCCCGGTGCNACCGNGGTGGGTCCGCGGATGGTNGGGTGTNCTCNNTACNGGAACGCCAGCGCN
ATCANCATCGGCANACTCNCGTGATGTGCCGCGGGCAACCATCCCCACAATGATCNGGTGCGTCTGATCAGGCN

(SEQ ID NO. 676)

Clone Rv8

.....Rv8SP6D.seq:.....
TTAGGCGTGACGGCCACCGGGGCACTCCGCACAATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTC
GCCGACTTTCGCGGGTACCCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCCGGC (SEQ ID NO. 677)

.....Rv8T7D4.seq:.....
CGTCACCCCGATGCGCCAGATCGGGGCTTCGCAGATAAAGCACGAACTGGCGGGCAAAACGTCGATCTCGGAGCCGG
AAGGGCAATCAGCCGACCGTCGACGAACGACACCGGCGAGACCACTTAGGCAGTGACGGCCT (SEQ ID NO. 678)

Clone Rv90

.....Rv90SP6.seq:.....
CTTTTCNCGATGTCTCATGATNCCNANGGAGAACNNTGCNANCNCNGCCGCTGACNTNGCNCACCGCTNTGGCNGNGG
TGACATTGGTGGTGGTTCGCGGGCTGCNACGCCCCGACTCGANGCCGANCCATNTNTTGGCGCCGACCGCNTNTCGTCTC
NACCGCANNNCCNATCTCNGCCGCNCCCGGTGGANCTACNGCTNCTTCGCCATCTCTCGCCNATGGCTCCNGCGNNTC
GCNCAACGTNTGGTTGGTNANCTGCCTACCTGGTCNT (SEQ ID NO. 679)

.....Rv90T7.seq:.....
GCTGCGCCAGTCGTTGCGGTGCGGTTCATGCCGTTGGACCNACCATCGGAGTTAGTTGCCGAACCGCGGACCACCGCAAG
CACCCGGTCTGGTTCGCGCACCAGCGTTCGGCCAAACCGCTTGAGCACCACACGCGCAGCCCTCGCCGCGCACGAATCC
ATCCGCGTTGGCGTCNAANCTGTNGCATCGGTTCGGTTCGGTGACAGCGCCGACCACTTGGACAGCGCGATGGCGGTGAA
CGGTNANTAGGTGACCTGCCNCCNCGCCCGCAATGCCACCTCCGCTTACNCATGCGAATGGTCTGACACGCCNAG
TGAATTGCCACCGAGCAACAAAAATCGGTATCTNCGCGACGGCGGACACGCNATCCNACTGATACTCGATCCGC
CCCACCGCTTGNANCTCCGGGTTCCNGTGCTCATGTACNTCATGTGCGTCTGCGCNCGATATTGACGATCGTGTTTC
CCACGANNANAGANCCTCATCACGCCGGTTCGAGTGCCG (SEQ ID NO. 680)

Clone Rv91

.....Rv91SP6.seq:.....
CTGTGTGCGGNCGGCGCGATATCGGCCTTTTACTAACCGAACCCGATGTGGGCTCCGATCCGGCGCGCATGGCATCT
ACNCGACGCCGATCGATGACGGCCAGGCTTACGAGCTTGAGGGTGTGAANTTGTGGACCNCCAACGGTGTGGTAGCG
GACCTGCTANTGGTTATGGCGCGGGTACCGCGCAGTGAANGGCACCGAGGGGGAATCANCGCCCTTGTCTGTCTANGCT
GATTCTCCCGGGATCACCNCTGGAGCGCNCNCNANTTTCATGGGACTGCGTGGCATCCAANACGGCGTGACCGGCTTCA
TCCNTCNGGGTGCCCAAAGACAACTTGATCNGCNGGGAAGCGACGTCTGAANATCGCGCTGATCNCACCTCAACGCCGG
ACGCTGTCTTACCGGCGATCGCACCGGANTTGCCAANCCGCGCTNANNATNCGCGNGAATGNCCGTCCACNANTGCAT
GG (SEQ ID NO. 681)

.....Rv91T7.seq:.....
TGGGGTGCCGGGCGCCGAGTTGCGTCCCTGGGATCACGCAGAGTCGCCGGCGGGTGGCGTTGGGCTATGAATTGCACC
GAGCCGGAATCCGCANCAAACTGCGAGTAGCGGCCTGCAGAAGTGCANCTCGGCGAAACGGAGTACGGTGGACA
ACGAAAGCGCCGGAACNACGCACTGGCCGAGGGATTGGCGTCAATCGGCCCCGCCGTCGAACTTGAAGANAC
ANTGCGGTTCTACCGTGATCTGGTGGGAATGCTCCAACNNACTTCNCCGAAAGCTACGGAAGCNACGGCGCGATNTT
CGGCCTTCCAGCTCGACCTGACGCTGGAAATCG (SEQ ID NO. 682)

Clone Rv92

.....Rv92SP6.seq:.....
NGGCNNGGAAGTTAATGCCCTACTGGTTCNATGCTCNACNTCNCNGTGACNNCTGCNCCGACCGCGCGAGGTCCCT
GNCCGTNACCACCGANCNGGCGATCCGGGACTCTNGTACGCATCCAACANNGANCAACGTGCACGGGCGGAGTNGTNC
CGCCACTTCGNCNATGACGGGGTTCGATCCNTTCGACGTCCGTGCGCCGCGTGGTTCGAGTGGCGGTACNCTCCNNGTA
CTCGACCNCACNGACGAGGAGTTCGANCCATCTACGTGTGGACGAAACANATCTTCTGTCCNACGACTACACCACC
ACCCAGGCCATCGCCGNCGCCCGCGANGCCCTTCGACGCCNTACTGGTCCNNGNGGNGCGCTCTCCGGTTGTCTNNC
NCNTGNCGTGTTCCCTTCACNCACTGCCCNACATCGANCCGAGCNATNCNANGTCCGTCAATC (SEQ ID NO. 683)

.....Rv92T7.seq:.....
GGACACTGTTCCGCTGCCCCCTCGTCAAAGCCGGAGTGGTCTGTGCTGCGCCGGACCCGACCCGACCTTCAGCGGGGGTT
CACAGCTCCGTGGGTGCCGTTACTTCCGATCGCCGCGAGTGTGCGCTGCCGTGGCTGATGCTGAACCTCACCGCGTT
GACTTGGATCCGGTTCGGGATCTGGCTGGTGGCCGGAACCGCGATTATGTGCTACGGGCGCCGCACTCGGCGCA
TGGCCTTCGGCAAGCNCNANANAACGCGACCCGGAGGTGTTGAACTAGCTTCGCCGCGTATTTACAAATTGCNTTATA
TGTCTACACATAAGACGCAAACTGCTCTATTGTCAANTCCANCCTGGTGTGGCNCATGAAGATGTTTGG

(SEQ ID NO. 684)

Clone Rv94

.....Rv94SP6.seq.....
TCCTTCTCGGTATCGGTTTGGGCTGTCACCANCAGTTGGTAGTTCTTCACGTNCTGTTGTTTCGAGCGTCNAGCCGTCG
CGCGTGTGNANGTCNCCGGACGCGTATCCCGCCAGGCCGGTCANGGTGCCCTTCCANTCCACGCCGCTGTGGTCGGCG
AACGCTNATCTTCAATCGAGACCATCGCCAGCTTCATCNTGTTGGCGATCTTGTCNNACGGCACCTCNAACCGGCGCT
NCTAGTACNCCACNCNATCNTGTTNCCTTCNCGTACATCCTCGATNCCNCNTGCACTTTCCCTCGANCNCCTGGGC
CGAGCCGTTGGCANTNACCTCNGAGCCCCATTGGACATCANCCANCCCGCTGCGAACGGGAACGTCAGCNCNCTGG
CGACAACCTGGCCAACAN (SEQ ID NO. 685)

.....Rv94T7.seq.....
CACNCCGTGATCGCNAGCCCCNGTAGAAATNGTTGAGCCAGTTGGTGCGGCGCTCGTTGCCGGCGGTNATCTCGTCGA
GCTCNTCTTCCATCGCCGCGGTGAAGTCGTACTCGACNAGCCGACCNAATGCTGCTCNAGCAGACCGGTTACNNNA
ACNCCNCTCNTGACNGCACCAGTGCNCTGCCCTTCTTGTCACGTACCCGCNATCCTGGATGGTCTTGATGATCNAC
TANTNTGTCGACGGGCGGCGGATGCCATCTCCTCNAGCGCTTTGACCAGCGACNCTCGGTGTATCGGGCGGCGGG
TTNGTGCGCATGGCCGTCTGGGGTCANCTCNACNATNTTCANCCGTTGACCCGGGGTCACA (SEQ ID NO. 686)

Clone Rv95

.....Rv95SP6.seq.....
TGGCTTCTTGNCANGGGCANNACATNNGCTATNGCGAGCGTGTAACCGATCATCNTCCNGGCGACTGTGGCCTGANCG
GCAAGGTNGCCTNATTCNTCCTCGNGGCATGGTTNCCACACGGAATGNCGGTAAGTCTGGTCGGCAACCTGGCCC
GCTGCCGGTTGGGTTTCGGATTTCGCTCGGCTANTAAAGTGCTCGCCTGGTGTNACNACTAATCNCNATATACTTANC
GGGAGTNGNCGTCCGATCCTNGCCCTGCCGCGGCGATCNCGTTCCGANACCCGCCACCGGAACCTCNAANGTGGCG
TCATCGGGCTCTACGCGCCATCTTCCCGGATTCTTCGCGGCGNGGTNCCGNGGGACCCCGGACTGTGACNGGCCCAA
CGGCTCATCATCG (SEQ ID NO. 687)

.....Rv95T7.seq.....
CCGGATAGCGGTGTCTGAACCTTCGCCCCTCCCTCCANCGCATTGAGCTTCAGCCCGACCGGCAGGTNNGGAGTCGGC
ATCGGGTCTTCGCCCCGACCCCGCTGGCTAAATANCCACCCCGAGCGCGGTACGGTCTTTGCACCGGGACGACGC
ATACCGGCAGCGCGAATCNCNCCGCGGCTGCAGCNTGAACGTCCAATACCANTCNAACAGTGTCCGCGCGTNAAAAC
CCGANCCGGCGGTTCGCTTCNGTAATCAACGGCTCCTGCGCAACCACTGCAAGTCCCGGTGCCACCGGCGTTGACGA
TCTTGATGTCTGCGANCTCGCGCACCAGCTCGACGGCCCGGGCA (SEQ ID NO. 688)

Clone Rv96

.....Rv96SP6.seq.....
CCTCCCGACCACATACAGGCAAAGTAATGGCATTACCGCGAGCCATTACTCCTACGCGCGCAATTAACGAATCCACCA
TCGGGGCAGCTGGTGTGATAACGAAGTATCTTCAACCGGTTGAGTATTGAGCGTATGTTTGGGAATAACAGGCGCAC
GCTTCATTATCTAATCTCCAGCGTGGTTAATCAGACGATCGAAAATTTATTGCAGACAGGTTCCCAAATAGAAAG
AGCATTTCTCCAGGCACAGTTGAAGAGCGTTGATCAATGGCCTGTTCAAAAACAGTTCTCATCCGGATCTGACCTTT
ACCAACTTCATCCGTTTCAGGTACAACATTTTTTAGAACCATGCTTCCCGAGGCATCCCGAATTTGCTCCTCCATCCA
CGGGGACTGAGAGCCATTACTATTGCTGTATTTGGTAAGCAAATACGT (SEQ ID NO. 689)

Clone Rv9

.....Rv9SP6.seq.....
CTTCACNTCCGTACGGCTCGGGTACGCTTCGGTCNCATTGTGCGAGTGATAGATGACGACCGGGACCTCGTCGGCATC
TTCCATAGCCCGCCACACCTTCAGTTGCTCACCGGAATCCAACCGGTANAAGGTCGGCGANCGCTCNGCATTGGTCAT
CGGGATATGCCGCTCGGGACGGTCANAGCCCTCGGGTCCGGCCAGCACTCCGCAGGCTTCGTCGGGGTGGTCGCGACG
CGCATGGGCCACCATCGCATTACCCAGGTCTGCGCGAATCACCAGCACGTANACGGTTCCTTTCTTAAGCAACACCGA
ANTTTTCAGGACCCGAATGCTCCGGGAAACATGTCACGGTAGGTGCGGTATTCCGGCTACCGGCTGANCATTGAGCACGC
CGGCCAGCACCGACGAACAGGCAATCAGCCGCCGCCGACCCGACCGCGG (SEQ ID NO. 690)

.....Rv9T7.seq.....
CAGGCATGCAAGCTTGATGCCGCCGAAACCGAGCGTGAGCACGCCGCCAGCCACCACGCGCGGGTCGGGCGCCGGGCC
CGGGCCGCGAGGCTGCTCCGCTCGGTGATGGCAGCCACCGCGACACCACCGGCTGCGCTACGTCGAGCCATACCGG
GCGGAGCTACATCGGCTCGGCGGCCAGTGTTGGGGCCCTCTTTCGAGGTCGAGGTCGATACCGATTGCGCATCCGC
AGCCGCACCTTGACGACAGAACCGTGCCCTACGAATTGCTTGTCGGGCGGGGCCAAAGAACAGATTGGCATCCTGGC
GCGATTGGCCGCGCGGCGCTGGTGCCAAGGAAGACCGGTTCCGGTGCTGAT (SEQ ID NO. 691)

RvXXXT7 corresponds to the T7 end-sequence of the clone RvXXX.

RvXXXIS 1081 corresponds to a region located close to a copy of the IS1081 repetitive sequence (Insertion element).

The character « - » denotes an uncertain base residue.

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.....X0001SP6.seq:.....

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TCGGGTTTCCACACGCGCGGTTTGACCCTAGTCATATGTAATCATGTGTACCATGTGCGGGCGCTTTTCGACGGCCG
CGAACCACCGGA-ATTTCTGTGATTTCACTGCATGCGTACCATCTGGACAATTGAGCA-TTGTCT-
TCGCGGTGGTCGG-CGGGTGCGTGCCGCCTGCTGCGA-ATGCACCA-
TAAGCCCGAACCACCGGCTTGGTGACCACCGCAGCTGCGTGTGGGGGTAACCACTCCGCGACCCCAAGGATGGT
CATTTCCAATGAACCGGCTGGACTTCGTCCA-A (250 bp, 222)

(SEQ ID NO. 692)

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:::X0001T7.seq:::

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GTGCGGGTTGATCGACCCGATCTTCACTCGTAACCTCGATGCTTAGCAGGATCCAGCTTGACCGCGTTTTGGCTCT
ACCCACTCTTTGAGTGGCGCCGTCGCTGTGCCCATCGGTGTTATGACGAACGCTTCGAAAGACTTCTCTTTGTG
AGCCCGGAATGTCTGCGTAAGAAGTTCATGTCTCGGGAAAGTAGACCCGGTGCCTTCCAGCTGGTACTCTCTCGAGG
TCCGCTTCTCGCCGATCCGATAAACACCGGCCCGAGGCACGCGAGCTGAGTTGCAACGCTTCAAGTAGGTTGTC
ATGCGGCGGACTCCGGGAGTGCAGAGAAATAGCGGTGCGCGTAGCTGTAGACCGGATGGTTTCCGCCAGGCTGACG
TCGAAGATGCCTCCTTGGAAGGGGCGCGA (SEQ ID NO. 693)

(SEQ ID NO. 693)

.....X0002SP6.seq.....

AACTCAAGTTTTTACGGTGATCGCGCATCACCTGGTTCATGAACTGGAAGCAGCGCAGCGCTTCTTTTTCGGCCGCA
ACATGAGCCAGCCTCTCGTCGGCGGTGCGGGTGCAGGTGCTCGGGCAGCTCGGCCGCGCAGCCGCCTGACCCTGAAA
CCAGCTTCCATATCCCGCGAC-
AACGACGCCAGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACAGCGCTTCTCCACCGACCAGGGCCCGGG
TGT (SEQ ID NO. 694)

(SEQ ID NO. 694)

.....X0002T7.seq.....

GTGCAGGTTTCGACAATGTGGTGCCGGTTTCGGCGGCTACGTGCCATCGAGACACTGGCGCA-GCTATCGCACCCGTT
ATCGGCTGCGAGCAAATCGCGGTATGCGTTCTTGAGCATGAGTCGGCGACCGTCGTATGGTCGACACCCACGACGG
AAAGACGCAGATCGCCGTC AAGCATGTGTGCCGCGGATTATCAGGACTGACCTCCTGGCTGACCGGCATGTTTGGTC
GCGATGCCTGGCGCCCGCGCGCTGGTCGTGGTCGGCTCGGATAGCGAGGTCAGCGAATTCTCGTGGCAGCTCGAA
AGGTCCTCGCCGGTGCCGGT

(SEQ ID NO. 695)

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.....X0003SP6.seq.....

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TTTCGAGTCATGCGCCCGCCTCGACCACGAA-ATGCACGTCG-

GGTTCGATCGACCCGATCTTCACCTCGTAACCTCGATGCTTAGCAGGATCCAGCTTGACCGCGTGGCTCTACCCA
CTCTTTGAGTGGCGCCGTGCGCTGTGCCCCATCGGTGTTTCATGACGAACGCTTCGAAAGACTTCCTCTTGAGCCG
GAATGTCTGCGTAAAGAAGTTCATGTCCGGGAAGTAGACCCGGTCGCCCTCCACGTGGTACTCCTTCGAGGTCCGC
TTCTC (SEQ ID NO. 696)

(SEQ ID NO. 696)

.....:X0003T7.seq:.....
GTCATGTGTACCATTTGCGGGCGCTTTTCGACGGCCGCGAAACACCGGAGATTTCTGTGATTTCACTGCATGCGTA
CCGTCTGGCACAATTGAGCAGTTGTCTGTGCGGGTGGTCGGCCGGGTTGCGTGCCGCCTGCTGCGAGATGCACCAAT
AAGCCCCGAACCCACCGGCTTGGTGACCACCGCACGCTGCGTGTGGGGGTAACCACGCCGCGACCCCAAGGATGGTC
ATTTCCAATGAACCGGCTGGACTTC-TCAACAA (SEQ ID NO. 697)

Clone X0004
.....:X0004T7.seq:.....
AACAGCGCGTTGAACTGATAGGTGCGGCCCGGCTCGAGCAGGCCGGGCCATTTGTTTCGATGCGGTTACCGAAAGAT
CTCTTCGGTGACCTGCCCGCCGCGCCAGCTCGGCCAGTGCCCGGCGTTGGCCGCCGCGGCGACGATCTTGGCGT
CCACGGTGGTTCGGGG (SEQ ID NO. 698)

Clone X0006
.....:X0006T7.seq:.....
GCATCTGGGCTGGCGGTGGTTTCGCCGCTCCGAAGCCGTGCAACACCATCGCCAGCGGGCTTCCACATCAACGACCA
TTTCGGCCAGCTTGC GGCGCATCAGCGGCTTGTTCGATGAGCGCCCCACCGAATGCCCGCCGCTGCCCGGCGTA-
CACAGCGATTTCGACCAGCGCGCGGCGCGCTTGCCGAGGGCGAACGAAGCGGTGCCCAACCGCAATCTGTTGGTCAG
CTCCATCATGCGGGTGAGTCCCTTGCCG (SEQ ID NO. 699)

Clone X0007
.....:X0007SP6.seq:.....
ATCGGTTTCCAGCAACAGCCGATCGACGGCTTCGCCCA-
GGCCGCTCCCGGGCGACCCGACCATTTGCTGTGCGCCGCGTAACGCCATCACGGATGACGCGCAGTTTCGTGCTGTCTA
GCTCCACCATCGCCTGCACACCGGGCGGCCAG-ACCCATTGGCCGTCGCACTCGTA-
AGCAGGTAATCCTCGTCGACGGACTCGGTAACCACCGCCGCGAGCTCCGCTGCCAGGTGCGCGGGGTTGACACCGGC
GGGCATCGGGATGGACGACGACGCGGTGCTGACGGCGCCTGTC (SEQ ID NO. 700)

.....:X0007T7.seq:.....
AGCGGTTTCCCA-
GCGGGATGTGCTGTGAGCGCCGCACCACCAGCGCCGACGCTAAGGATGGAACGCACGGCATCTTCTGACGCGTAACC
GCGTTGTGATCGCGAGCTGAGGAGACGGTATGGGGGAGGGTTCTCGGAGGCCATCTGGGATGTTGATGCTGTTCGAT
CTTGAGCCGGTGCAACTCGTCGGCCCGGACGGTACGCCGACGGCCGAACGCCGCTACCACCGTGACCTTCCTGAGGA
AACGCTGCGTTGGCTCTACGAGATGATGGTGGTCACCCGCGAGCTGGATACCGAATTCGTCAATCTGCACG
(SEQ ID NO. 701)

Clone X0008
.....:X0008SP6.seq:.....
CAAGCTTCCACAGGTAGGGATCGAGGAACAGCGGTTGAACTGATAGGTGCGGCCCGGCTCGAGCAGGCCGGCCATT
TGTTTCGATGCGGTTACCGAAAATCTCTTCGGTGACCTGCCCGCCGCGGCCAGCTCGGCCAGTGCCCGGCGGTTGGC
CGCCGCGGCAACGATCTTGGCGTCCACGGTGGTTCGGGGTCATGCCCGCGAGCAGGATCGGCGAGCGCCGGTCAGCC
GGGTGAACTTCGTGAAAGCTTGACCCTGCCGTGCGGGAGGCGAACCACGGTCGGTGCGTANCTCCACCAAGCCCGG
GCAACCTCGGGGGTGGCGCC (SEQ ID NO. 702)

.....:X0008T7.seq:.....
TGGACCTCATGACAACGCGGGCGGCGATTACCCCCGTACCGCCAGCAGCATGACGGCGGTAGCGAACACCGCCGGAT
GCAGCGCAGGTGCGTCGATGTGCTCACGGAATCGCCCCGGCACCGCGATCTCGAGGATCACCAGTGCCACCCCTGC
AGCGCGACACCGACGATTCCTGACACCGCCACCGCGATCAGGCCCTGGGCCAGCTGGCGTATATGGCGGCGATGGTG
ACGATGGCCAGCGCCACATACATTGTGGCGGGCAGAACCACGGCGTTGGGGCGGGCGGTGATGAACACTAGGCGACG
CAGATCGCCCGGGGTCAACAGGTTGACCATCAGAAAGCCTGCGA (SEQ ID NO. 703)

Clone X0009
.....:X0009SP6.seq:.....
TTTGGTGCGGCCGGCAATCAACTTC-GCTC-
CAGCGGTTTCCCAGGCGGGATGTGCTGTGAGCGCCGCACCACCAGCGCCGACGCTAAGGATGGAACGCACGGCATCT
TCTGACGCGTAACCGGTTGTGATCGCGAGCTGAGGAGACGGTATGGGGGAGGGTTCTCGGAGGCCATCTGGGATGT
TGATGTCTGTTCGATCTTGAGCCGGTGCAACTCGTCGGCCCGGACGGTACGCCGACGGCCGAACGCGCTACCACCGT
GACCTTCCTGAGGAAACGCTGCGTTGGCTCTACGATATGATGGTGGTCACCCG (SEQ ID NO. 704)

.....X0009T7.seq:.....
CGCCCAGGGCCGCTCCCGGGCGACCCGACCATTGCTGTCGCCGCGTAACGCCATCACGGATGACGCGCAGTTTCGTCTG
CTGCTAGCTCCACCATCGCCTGCACACCGGCGGCCAGGACCCATTGGCCGTCGCACTCGTAGAGCAGGTAATCCTC
GTCGACGGACTCGGTAACCACCGCCGCGCAGCTCCGCTGCCAGGTCGGCGGGGTTGACACCGGCGGGCATCGGGATGG
ACGACGACGCGGTGCTGACGGCGCTGTCGCGACGCTGAGCTCGGACACAGCTAGTAAATGTAGCCTAACCTACTTA
ATGGGTGCGAGCCCCCGGGGTCGTGCGATGTCCAACGTTGCTCGACTGGAAGAAAATGCTCGTCGGGGAGCAAATG
GCACC (SEQ ID NO. 705)

Clone X0010

.....X0010SP6.seq:.....
AATACTCAATCTTGATCGGTTTCCAGCAACAGCCGATCGACGGCTTCGCCAGGGCCGCTCCCGGGCGACCCGACCA
TTGCTGTCGCCGCGTAACGCCATCACGGATGACGCGCAGTTTCGTGCTGCTAGCTCCACCATCGCCTGCACACCGG
CGGCCAGGACCCATTGGCCGTCGCACTCGTAGAGCAGGTAATCCTCGTCGACGGACTCGGTAACCACCGCCGCGCAGC
TCCGCTGCCAGGTGCGCGGGGTTGACACCGGCGGGCATCGGGATGGACGACGACGCGGTGCTGACGGCGCCTGTGCG
GACTCTGAGCTCGG (SEQ ID NO. 706)

.....X0010T7.seq:.....
GGATGTGCTGTGAGCGCCGACCAACAGCGCCGACGCTAAGGATGGAACGCACGGCATCTTCTGACGCGTAACCGCG
TTGTGATCGCGAGCTGAGGAGACGGTATGGGGGAGGGTTCTCGGAGGCCATCTGGGATGTTGATGTCTGTCGATCTT
GAGCCGGTGCAACTCGTCGGCCCGGACGGTACGCCGACGGCCGAACGCCGCTACCACCGTGACCTTCTGAGGAAAC
GCTGCGTTGGCTCTACGAGATGATGGTGGTCACCCGCGAGCTGGATACCGAATTTCGTCAATCTGCAGCGCCAGGGGG
AAGCTGGCGTTGTACACGCCCTGTGCGGGCAGGAAGCCGCGCAGGTGGGTGCGGGGCTTGCTACGAAAACCGA
CTGGTTGTTCCCC (SEQ ID NO. 707)

Clone X0012

.....X0012SP6.seq:.....
ATCACGACAACAGCGACGGTGTGTCGGATCAGCGGCCCCCGTTGCCGGGCAATGTTGAGGCGTTTCTGCGTCTGGTT
GAGCCCGCTGGGAC-
CCGAGGTGGCTCGTCGGCCACATGGGCAGCACACCACCGTGGTGATGCATCTAGACGTGCAGGACCGTGCCGCTGGC
CTGCA (SEQ ID NO. 708)

.....X0012T7.seq:.....
GCGGCTACGTGCCATCGAGACACTGGCGCAGGCTATCGCACCCGTTATCGGCTGCGAGCAAATCGCGGTATGCGTTT
TTGAGCATGAGTCGGCGACCGTCTGTCATGGTCGACACCCACGACGGAAGACGCAGATCGCCGTCAAGCATGTGTGC
CGCGGATTATCAGGACTGACCTCCTGGCTGACCGGCATGTTTGGTCGCGATGCCTG: (SEQ ID NO. 709)

Clone X00013

.....X0013T7.seq:.....
TACAAGCGGCACCTCGCCGGTGAACGTGACCGTTTCGCACGCTGCGCACCGCCGCCGGGCGCGTGCTCGGCGCGCCGGC
GGCCCCGAGGCTGAGAGGGGAACCAACCATGCAGGTGAACATGACGGTAAACGGCGAGCCCGTCACCGCCGAGGT
CGAACCCCGGATGCTGCTGGTCCATTTTCTCCGTGATCAGCTGCGGCTCACCGGAACTCACTGGGGCTGTGATACCA
GCAACTGCGGGACATGCGTGGTGGAGGTGACGCGCGTGCCGGTGAATCCTGCACGATGCTCGCCGTGATGGCCTCC
GGGC (SEQ ID NO. 710)

Clone X0014

.....X0014T7.seq:.....
AGCGGCTGGTTACGACTCCCTGTTGTGATGGACACTTCTACCAACTGCCCATGTTGGGGACGCCCG-CC-
TCCGATGCTGGAAGCCTACACTGCCCTTGGTGCGCTGGCC-C-GCGACCGAGCGGCTGCAACTGGGCGC-
TTGGTGACC-GCAATACCTACCGCACCC-ACCCTGCTGG-CAAA-
ATCATACCACGCTCGACTTGTTAGCGCCGGTCTGA-CGATCCTCGGCATTGGAACCGGTTGGTTT-
(SEQ ID NO. 711)

Clone X0015

.....X0015SP6.seq:.....
ACGCGCGCGATCATATCTGCTATGGATGTACAATTCAGCTCTTGCTGTTATACCAGTATATGGTGTACTATTTGAT
CTATGCTGACGTGTGAGATGCGGGAATCGGCCCTGGCTCGACTCGGCCGGGCTCTGGCTGATCCGACGCGGTGCCGG
ATTCTGGTGGCGTTGCTGGATGGCGTTTGCTATCCCGGCCAGCTAGCTGCGCACCTCGGGTTGACCCGATCGAATGT
GTCCAACCATCTGTCTGTTTGGGGGGCTGCGGGCTGGTA-TCCCAACCTATGAGGGCCGGCAGGTTCCGTAT
(SEQ ID NO. 712)

.....X0015T7.seq.....
CCGCGCTGCTGCTGACGTGCGTTCGAACGTGCGACACGTCTGCGAATACCGGCCGAACGCTGGGTTTATCCACAGGCT
GGCACCAGCGCCACGACACACCGGCCGTCGCCGACCGCCACCGACTGCATCGGTTCGACGGCCATTCGGATCGCCGG
TGCCCGGGCGCTGGAACGTGGCTGGGCTGGGGCTCGATGACATCGAATACGTTCGACCTGTATTTCGTGCTTTCCCTCCG
CTGTCCAAGTCGCCGCAATCGAACTCGGCCTGGACACCGACGATCCTGCCCGCCGCTGACCCTCACCGGGGGCCTG
ACCTTCGCCGGCGGGCCGTGGAGCAATTACGTACGCACTCCAT (SEQ ID NO. 713)

Clone X0016
.....X0016SP6.seq.....
CAGGCGTGCAATGACCTGCACTGCGCCGGA-A-
TCCCTAACCCACTAAACCGGGGCCGCTCACAAGCCGTGCAGCTCGGTGAGCGTCAGGTGCGCGACCAGGAA-
TAAATGAGCAGACCCGTGCCGTCAACGATGGTGGCGATCATCGGCCCGAAACGATGGCCGGGTC-
ATGCGCAACTTCTTCAGCAGCGGCGGAAGGACGGCA-CCACCAGCGAC-ACCACACCACGAT (SEQ ID NO. 714)

.....X0016T7.seq.....
GCGAA-
CACTTCGTCAACTTCAGGGCTGCCCGCACCAAGTATTTTCGACGAGTATTTCCGTGCGGGCCGCCGCCCGGGCGCGC
GGCAGGTGGTCATCCTGGCGCGGGGGCTGGACTCGCGCGCGTACCGGCTGCCTTGGCCCCGACGGGACCACGGTTTTT
GAGCTGGACCGCCCGCAGGTCCTTGATTTCAGCGCGAGGTGCTCGCCAGCCACGGTGCCCAACCGCGCGCCCTGCG
CCGCGAGATCGCCGTGACCTGCGTGACGATTGGCCACAAGCCTTGCGGGACAGTGGTTTCGATGCGGCTGCACCGT
CGGCATGGATTGCCGAAGGGCT (SEQ ID NO. 715)

Clone X0017
.....X0017SP6.seq.....
TTGGGC-TTGGCC-CAATA-GGCCCAATCAAAAGCCGAGCAGGTGGAACCTA-CGCATTGCGCTC-TCGT-
TGTGCACCCGAGCCATCGCACGCGCGGAATTCCCGGAT-TC-
CCGTATTCTCCGGCGGGCGGGCTAACCCATCCCA-GCCGAACGGTTGGCTC-
TGCCGTGGGTCCCGTGTGGCCGATCGGGGCGTCACCGGGGGTGCTCGGGTGCGG-TGACCATGGC-AACTGCCCC-
ATGGGCCGACCTGGTGCAGATAAACCTG (SEQ ID NO. 716)

.....X0017T7.seq.....
TGGTGGAGGTCCCCACCAA-ACCCGGCCGTAACCTCTGTCACGGAAATGCGG-
CAGGCCGCGCTAGCACGTGGTATCCGCCATAAAGGTGCACCTTAAGCACGGCGTCCCAATTCTCGAACGACATCTT
GTGGAAGGTGCCGTGCGCAAGATCCCGGCGTTGCTCACCACACCGTGACGGCGCCGAATTCTGCAAGCGCGGTCT
TGATGATGTTGCTGCGCCGTCCTCGGTGGCGACGCTGTCGGTA-
TTGGCGACCGCCCGGCCCCCTTGTGCGGAAATCTCGGCGACGACCTCATCGGCCATCGCCGAACCGGGCGCCCC
(SEQ ID NO. 717)

Clone X0018
.....X0018SP6.seq.....
GCCGGCCAACTGGCCGGCGGGTTGCTGTC-TCAAGGTGGGTTCCGCCACCAA-ACC-
CACTCAAGGATCGCAAGGAAAGC-
TCAAGGATGCGGTGCGGGCCGCCAAGGCCGCGGTCAAGGAGGGCATCGTCCCTGGTGGGGGA-
CCTCCCTCATCCACAGGCCCGCAAGGCGCTGACCGAACTGC-TGCGTC-C-GACCGGTGACAA-
GTCCTCGGTGTCCACGTGT-CTCCGAAGCCCTTGGCGCTCCGTTGTTCTGGATC-CC-CCAAC-
CTGGCTTGGACGGCTC-GTGGTGGTCAACAAGGTGACGAGCTACCCGCCGGGCATGGGCTGAACGTGA
(SEQ ID NO. 718)

Clone X0018
.....X0018T7.seq.....
CGAACCT-AATTGTCCTGTAATGCCAGCTACCAA-
GCATGGCTGGTGGCCGGGCGGTGAAGCCGGCGTCTGCGGCACCGTCCAACTC-ATGTGGAT-
GCCGGAATGGGGATGTCCGG-ACGGCGAATCCGTA-
TTCGCTTGTCCCGTGAGGCCAGGTGGATGGGGGAAGGATC-TGGTGTCCGGGATGAT-
ATGGGGCCGATGCCGCCGTTGAAGTCCACTGGATCGGGAATCGGGAATCGTGAT-CCGACGTTTCAGGCCGAAC
(SEQ ID NO. 719)

Clone X0019

.....X0019SP6.seq:.....
CTAACGGAATGAAAGCCCTGGTGGCCGT-
TCGGCGGTGGCCGTCGTCGCACTGCTCGGTGTATCTTCGCCCAAGCTGATCCCGAGGCGGATCCCGGCGCAGGTGA
GGCCAATATGGTGGCCCCCAAGTTCACCGTCTTGTGATCACACCGAATGGGCGCA-
TGGGGAATTCTGCCAGCCTCCGGGTCTACCGTCCCAAGTTGGGCGTACA-
CCTCCCGCCGCTCGGGATGGCCGCTGCCGACCCGGCCTGGGCC-
AGGTTCTCGCGCTGTACCGGAAGCCGACACTGCCGGC (SEQ ID NO. 720)

.....X0019T7.seq:.....
CCGCGGGACAC-CCTC-
ATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGGAACGCTTCGCCCGGGG
CGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTTCGATGACGGCATCGCCACCGGAGCGACGGCCAAGGC
GGCGTGCCAGGTGCCCGGGCGCACGGTGCGGACAAGGTGGTGTGGCGGTCCCGATCGGCCCA-
ACGACATCGTGGCGAAGATTCGCCGGGTACGCCGATGATGTGGTGTGTTGGCGACGCCGGCGTTGT
(SEQ ID NO. 721)

Clone X0020

.....X0020T7.seq:.....
CTCTGGGACCGGCCACGGTGCC-
CCGGCGTTCCCGGACGTGCTGCGCCAGGTGTCCGGCGGCCGCGTGCATGGTGTTCGCCGATCGGCCGCTGGCCAGAG
CCCACCGGTGAATCTGGCGCCTGGCCGACCACCGTGCGCCGTAGGCTTGCATCGTGCAGCGCTGGCGTGGCCAGGA
CGAGATCCCGACGGATTGGGGCAGATGCGTGCTCACCATCGGGGTATTTGACGGCGTGCACCGCGGGCACGCCGAAC
TGATCGCGCACGCGGTCAAAGCGGC (SEQ ID NO. 722)

Clone X0021

.....X0021SP6.seq:.....
AATACTCAAGCTTTCGTCACTTCATTGCGCCAGCAGACCAACAA-AGCATCGGGACATACGGA-
TCAACTACCCGGCCAACGGTGATTTCTTGGCCGCCGCTGACGGCGCGAACGACGCCAGCGACCAC-
TTCAGCAAATGGCCA-CGCGTGCCGGGGCCACGAGGTGGTGTCTCGGCGGCTACTCCAGGGTGCGGCGGTGATC-
ACATC-TCACCGCCGCACCACTGCCCGGCCCTCGGGTTACGCGAGCCGTTGCCGCCCGCAGCGGAC-
ATCACATCGCCGCGATCGCCCTGTTCCGGGAATCCCTC-GGCCGCGCTGGCGGGCTGATTAAC (SEQ ID NO. 723)

.....X0021T7.seq:.....
TGCCGCGGATTTGGCTGGCTGCCCAATATTGAGATCGGGCCTTTCTTTTTCGCGGACAATAAGGTCACAGTAAACC
CTCGTTTGTGAGATGCGGGGCGGGGCCGGCGAA-
TCGACCTCGAGTGAATGGATCTCGAGTGAATGGACAGGGCATCGCCTACGAGTCGCATCCCATCCAACAGACCGGT
GCTCTGTCATCGGACCTGAAGGTCCCGCACGGAGGGTGTGGTTGCCGGCGCGGGGTACCGGTGCGGTAGCGACGTA
GTGTTGAACGAATTTCTTGATGCTCAACCTGTTGGTGTTCATCCAGTTCT (SEQ ID NO. 724)

Clone X0175

.....X0175SP6.....
AA-CTTGCGCGCTCGGCCGGGTC-AGCATCCAGCTGCTCGGCAAGGAGGCCAGCTAC-C-
TCGTCGCTATGCCAGCGGTGAGATCCGCCGGGTC-
ACGTCCGCTGCCGCGCACCGTCCGGCAAGTGGGCAATGCCGAGCAGGCAAACATCAACTGGGGCAAGGCCGGTCGG
ATGCGGTGGAAGGGCAAGCGCCCGTCCGTCCGGGGCGTGGTGAT-AACCCGGTC-
ACCACCGCACGGCGGTGGTGAAGGTAAAACCTCCGGCGGCCGTACCCGTTAGCCCGTGGGGCAA
(SEQ ID NO. 725)

.....X0175T7.....
A-TCGAAAGTGACCATCTACCTTGAGTGCCATACCGCCGACCCATGCTCGGATAGCTCGGCGGAAAGAAACG
CTTGCACTGCCCGCAATAGCGGGCTACGTCGTGAGCGCCCATCAACTCTCGCGCGGAGTGATCGCCAGCTGGGCG
GCGCCGACGTCGACCGTGGGGATTCCGGTGCGCGCGCGGCCAACGGCCCGATCGTCGACCCGCACGGCAGATCGGC
GCGATGTTGTAACGCTGCATAGGCACTCCCGCGCGCTGGCAGGCCAGTGCGAACGCCCGCGCGGTGCGTCCG
(SEQ ID NO. 726)

References :

- Altschul, S. F., W. Gish, W. Miller, E. W. Myers, and D. J. Lipman. 1990. Basic local alignment search tool. *J. Mol. Biol.* **215**:403-10.
- Balasubramanian, V., M. S. Pavelka, Jr., S. S. Bardarov, J. Martin, T. R. Weisbrod, R. A. McAdam, B. R. Bloom, and W. R. Jacobs, Jr. 1996. Allelic exchange in *Mycobacterium tuberculosis* with long linear recombination substrates. *J. Bacteriol.* **178**:273-279.
- Barany F., 1991, *Proc. Natl. Acad. Sci. USA*, **88**:189-193.
- Bensimon, A., A. Simon, A. Chiffaudel, V. Croquette, F. Heslot, and D. Bensimon. 1994. Alignment and sensitive detection of DNA by a moving interface. *Science*. **265**:2096-2098.
- Bergh, S., and S. T. Cole. 1994. MycDB: an integrated mycobacterial database. *Mol. Microbiol.* **12**:517-534.
- Bimboim, H. C. and J. Doly. 1979. A rapid alkaline extraction procedure for screening recombinant plasmid DNA. *Nucleic Acids Res.* **7**:1513-1523.
- Burg J.L. et al., 1996, *Mol. and Cell. Probes*, **10**:257-271.
- Cai, L., J. F. Taylor, R. A. Wing, D. S. Gallagher, S. S. Woo, and S. K. Davis. 1995. Construction and characterization of a bovine bacterial artificial chromosome library. *Genomics*. **29**:413-425.
- Canard, B., and S. T. Cole. 1989. Genome organization of the anaerobic pathogen *Clostridium perfringens*. *Proc. Natl. Acad. Sci. USA* **86**:6676-6680.
- Chu B.C.F. et al., 1986, *Nucleic Acids Res.*, **14**:5591-5603.
- Chuang S. et al., 1993. Global regulation of gene expression in *Escherichia coli*. *J. Bact.*, **175**(7) : 2026-2036.
- Chuang, S., D. L. Daniels, and F. R. Blattner. 1993. Global regulation of gene expression in *Escherichia coli*. *J. Bacteriol.* **175**:2026-2036.
- Cole, S.T., R. Brosch, K. Eiglmeier, T. Garnier, S. V. Gordon, C. Churcher, D. Harris, K. Badcock, D. Basham, D. Brown, T. Chillingworth, R. Connor, R. Davies, K. Devlin, T. Feltwell, S. Holroyd, S. Gentles, K. Jagels, J. McLean, S. Moule, L. Murphy, K. Oliver, J. Osborne, J. Parkhill, M. Quail, M-A. Rajandream, J. Rogers, S. Rutter, K. Seeger, J. Skelton, R. Squares, S. Squares, J. Sulston, K. Taylor, S. Whitehead and B.

- G. Barrell. 1997. Genome Sequence of *Mycobacterium tuberculosis* H37Rv. *Microbial Comparative Genomics*, 2:174.
- Collins, D. M., and D. M. Stephens. 1991. Identification of an insertion sequence, IS1081, in *Mycobacterium bovis*. *FEMS Microbiol. Lett.* 67:11-15.
- 5 Cousins D. et al., 1998, 36(1) : 168-170.
- De Wit D. et al., 1990, *J. Clin. Microbiol.*, 28 : 2437-2441.
- Dear, S., and R. A. Staden. 1991. Sequence assembly and editing program for the efficient management of large projects. *Nucleic Acids Res.* 19:3907-3911.
- Duck P. et al., 1990, *Biotechniques*, 9:142-147.
- 10 Guateli J.C. et al., 1990, *Proc. Natl. Acad. Sci. USA*, 87:1874-1878.
- Kievitis T. et al., 1991, *J. Virol. Methods*, 35:273-286.
- Kim, U. J., B. W. Birren, T. Slepak, V. Mancino, C. Boysen, H. L. Kang, M. I. Simon, and H. Shizuya. 1996. Construction and characterization of a human bacterial artificial chromosome library. *Genomics*. 34:213-218.
- 15 Kwoh D.Y. et al., 1989, *Proc. Natl. Acad. Sci. USA*, 86:1173-1177.
- Landegren U. et al., 1988, *Science*, 241:1077-1080.
- Liu, Y. G., and R. F. Whittier. 1995. Thermal asymmetric interlaced PCR: automatable amplification and sequencing of insert end fragments from P1 and YAC clones for chromosome walking. *Genomics*. 25:674-681.
- 20 Lizardi P.M. et al., 1988, *Bio/technology*, 6:1197-1202.
- Matthews J.A. et al., 1988, *Anal. Biochem.*, 169:1-25.
- Michalet, X., R. Ekong, F. Fougerousse, S. Rousseaux, C. Schurra, N. Hornigold, M. Vanslegtenhorst, J. Wolfe, S. Povey, J. S. Beckmann, and A. Bensimon. 1997. Dynamic molecular combing - stretching the whole human genome for high-resolution studies.
- 25 *Science*. 277:1518-1523.
- Misumi, D. J., D. L. Nagle, S. H. McGrail, B. J. Dussault, Jr., J. S. Smutko, H. Chen, O. Charlat, G. M. Duyk, C. Ebeling, L. Baldini, G. A. Carlson, and K. J. Moore. 1997. The physical and genetic map surrounding the *Lyst* gene on mouse chromosome. *Genomics*. 40:147-150.

- Pavelka, M. S., Jr., and W. R. Jacobs, Jr. 1996. Biosynthesis of diaminopimelate, the precursor of lysine and a component of peptidoglycan, is an essential function of *Mycobacterium smegmatis*. *J. Bacteriol.* **178**:6496-6507.
- Philipp, W. J., S. Nair, G. Guglielmi, M. Lagranderie, B. Gicquel, and S. T. Cole. 1996a. 5 Physical mapping of *Mycobacterium bovis* BCG pasteur reveals differences from the genome map of *Mycobacterium tuberculosis* H37Rv and from *M. bovis*. *Microbiology.* **142**:3135-3145.
- Philipp, W. J., S. Poulet, K. Eiglmeier, L. Pascopella, V. Balasubramanian, B. Heym, S. Bergh, B. R. Bloom, W. R. Jacobs, Jr., and S. T. Cole. 1996b. An integrated map of the 10 genome of the tubercle bacillus, *Mycobacterium tuberculosis* H37Rv, and comparison with *Mycobacterium leprae*. *Proc. Natl. Acad. Sci. USA.* **93**:3132-3137.
- Poulet S. et al., 1995, *Arch. Microbiol.*, **163** : 87-95.
- Ross BC, 1992, *J. Clin. Microbiol.*, **30** : 942-946.
- Sambrook, J., E. F. Fritsch, and T. Maniatis. 1989. *Molecular cloning: a laboratory* 15 *manual*, 2nd ed. Cold Spring Harbor Laboratory, NY: Cold Spring Harbor. N. Y.
- Sanchez-Pescador R., 1988, *J. Clin. Microbiol.*, **26**(10):1934-1938.
- Segev D., 1992, in « Non-radioactive Labeling and Detection of Biomolecules ». Kessler C. Springer Verlag, Berlin, New-York, 197-205.
- Sheng, Y., V. Mancino, and B. Birren. 1995. Transformation of *Escherichia coli* with 20 large DNA molecules by electroporation. *Nucleic Acids Res.* **23**:1990-1996.
- Shinnick T.M. et al., 1987, *J. Bact.*, **169**(3) : 108-1088.
- Shizuya, H., B. Birren, U. J. Kim, V. Mancino, T. Slepak, Y. Tachiiri, and M. Simon. 1992. Cloning and stable maintenance of 300-kilobase-pair fragments of human DNA in *Escherichia coli* using an F-factor-based vector. *Proc. Natl. Acad. Sci. USA.* **89**:8794- 25 8797.
- Spargo C.A. et al., 1996, *Mol. and Cell. Probes*, **10**:247-256.
- Stone B.B. et al., 1996, *Mol. and Cell. Probes*, **10**:359-370.
- Trieselman B.A. et al., 1992. Transcriptionally active regions in the genome of the archaeobacterium *Haloferax volcanii*. *J. Bact.*, **174** : 30-34.
- 30 Trieselmann, B. A., and R. L. Charlebois. 1992. Transcriptionally active regions in the genome of the archaeobacterium *Haloferax volcanii*. *J. Bacteriol.* **174**:30-34.

- Urdea M.S. et al., 1991, Nucleic Acids Symp. Ser., 24:197-200.
- Urdea M.S., 1988, Nucleic Acids Research, 11: 4937-4957.
- Van Soolingen D., 1993, J. Clin. Microbiol., 31 : 1987-1995.
- Willets, N., and R. Skurray. 1987. Structure and function of the F-factor and mechanism
5 of conjugation. In *Escherichia coli and Salmonella Typhimurium: Cellular and Molecular
Biology* (F.C. Neidhardt, Ed) Vol.2 pp1110-1133, Am. Soc. Microbiol., Washington,
DC.
- Woo, S. S., J. Jiang, B. S. Gill, A. H. Paterson, and R. A. Wing. 1994. Construction and
characterization of a bacterial artificial chromosome library of *Sorghum bicolor*. Nucleic
10 Acids Res 22:4922-4931.
- Zimmer, R., and A. M. V. Gibbins. 1997. Construction and characterization of a large-
fragment chicken bacterial artificial chromosome library. Genomics. 42:217-226.

CLAIMS

1. A method for isolating a polynucleotide of interest that is present in a genome of a first mycobacterium strain or that is expressed by said first mycobacterium strain and that is absent or altered in a genome of a second mycobacterium strain that is different from the first mycobacterium strain or that is not expressed in the second mycobacterium strain, said method comprising:
- 5 a) contacting under hybridizing conditions the genomic DNA of the first mycobacterium strain with the DNA of at least one clone that belongs to a bacterial artificial chromosome (BAC) genomic DNA library of the second mycobacterium strain ; and
- 10 b) isolating the polynucleotide of interest that fails to form a hybrid with the DNA of the second mycobacterium strain.
2. The method according to claim 1, wherein the BAC-based DNA library
- 15 has been constructed from genomic DNA of *Mycobacterium tuberculosis*.
3. The method according to claim 2, wherein the BAC-based DNA library has been constructed from genomic DNA of *Mycobacterium tuberculosis* strain H37Rv.
4. The method according to claim 3, wherein the BAC-based DNA library
- 20 has been deposited in the Collection Nationale de Cultures de Microorganismes (CNCM) on November 19, 1997 under the accession number I-1945.
5. The method according to claim 1, wherein the BAC-based DNA library has been constructed from genomic DNA of *Mycobacterium bovis*.
6. The method according to claim 5, wherein the BAC-based DNA library
- 25 has been constructed from the genomic DNA of *Mycobacterium bovis* BCG strain Pasteur.
7. The method according to claim 6, wherein the at least one BAC-based DNA library has been deposited in the Collection Nationale de Cultures de Microorganismes (CNCM) on XX XX, 1998 under the accession number I-
- 30 XXXX.
8. A method of isolating a polynucleotide of interest that is present in a genome of a first mycobacterium strain or that is expressed by the first mycobacterium strain and that is absent or altered in a genome of a second mycobacterium strain or that is not expressed by the second mycobacterium strain, said method comprising :
- 35

- a) providing at least one polynucleotide contained in a clone of a bacterial artificial chromosome (BAC) DNA library of the first mycobacterium strain;
b) providing at least one genomic or cDNA polynucleotide from a second mycobacterium strain that is different from the first mycobacterium strain or at
5 least one polynucleotide contained in a clone of a BAC DNA library prepared from the genome of the second mycobacterium strain;
c) contacting under hybridizing conditions the polynucleotide of step a) with the polynucleotide of step b); and
d) isolating the polynucleotide of step a) that has not formed a hybrid complex
10 with the polynucleotide of step b).

9. The method of claim 8, wherein the polynucleotide contained in a clone of a BAC DNA library of the first or second mycobacterium strain is prepared by the following procedure :

- 1) digesting at least one recombinant BAC clone by an appropriate restriction
15 endonuclease to yield a polynucleotide insert of interest; and
2) isolating the polynucleotide insert of interest.

10. A purified polynucleotide of interest that has been isolated according to the method of claim 8.

11. The purified polynucleotide of claim 10 which contains at least one
20 Open Reading Frame (ORF).

12. The purified polynucleotide of claim 11, which is SEQ ID N0:1.

13. The purified polynucleotide of claim 11, wherein said polynucleotide is selected from the group consisting of :

- a) a polynucleotide comprising at least 8 consecutive nucleotides of SEQ ID
25 N0:1 ;
b) a polynucleotide having a sequence fully complementary to SEQ ID N°:1 ; and
c) a polynucleotide that hybridizes under stringent hybridization conditions with the polynucleotide defined in a) or with the polynucleotide defined in b).

14. The purified polynucleotide of claim 13, which is SEQ ID N0:2.

- 30 15. The purified polynucleotide of claim 13, which is SEQ ID N0:3.

16. The purified polynucleotide of claim 11, wherein the ORF encodes all or part of a polypeptide involved in the pathogenicity of a mycobacterium strain.

17. The purified polynucleotide of claim 11, wherein the ORF encodes all or part of a Polymorphism Glycine Rich Sequence (PGRS).

18. The purified polynucleotide of claim 17, which is SEQ ID N0:4.

19. The purified polynucleotide of claim 17, which is selected from the group consisting of :

a) a polynucleotide comprising at least 8 consecutive nucleotides the of SEQ ID N0:5 ;

b) a polynucleotide having a sequence that is fully complementary to SEQ ID N0:5 ;

c) a polynucleotide that hybridizes under stringent hybridization conditions with the polynucleotide defined in a) or with the polynucleotide defined in b).

20. A pair of the purified polynucleotides as claimed in claim 10.

21. A *Mycobacterium tuberculosis* strain Rv37 genomic DNA library that has been deposited in the Collection Nationale de Cultures de Microorganismes under accession number I-1945, wherein said genomic DNA library comprises recombinant bacterial artificial chromosome vectors.

22. A recombinant bacterial artificial chromosome (BAC) vector, which belongs to the genomic DNA library of claim 21.

23. The recombinant BAC vector of claim 22, which is selected from the group consisting of :

Rv101; Rv102; Rv103; Rv104; Rv105; Rv106; Rv107; Rv108; Rv109; Rv10;
Rv110; Rv111; Rv112; Rv113; Rv114; Rv115; Rv116; Rv117; Rv118; Rv119;
Rv11; Rv120; Rv121; Rv122; Rv123; Rv124; Rv126; Rv127; Rv128; Rv129;
Rv130; Rv132; Rv134; Rv135; Rv136; Rv137; Rv138; Rv139; Rv13; Rv140;
Rv141; Rv142; Rv143; Rv144; Rv145; Rv146; Rv147; Rv148; Rv149; Rv14;
Rv150; Rv151; Rv152; Rv153; Rv154; Rv155; Rv156; Rv157; Rv159; Rv15;
Rv160; Rv161; Rv162; Rv163; Rv164; Rv165; Rv166; Rv167; Rv169; Rv16;
Rv170; Rv171; Rv172; Rv173; Rv174; Rv175; Rv176; Rv177; Rv178; Rv179;
Rv17; Rv180; Rv181; Rv182; Rv183; Rv184; Rv185; Rv186; Rv187; Rv188;
Rv18; Rv190; Rv191; Rv192; Rv193; Rv194; Rv195; Rv196; Rv19; Rv1; Rv201;
Rv204; Rv205; Rv207; Rv209; Rv20; Rv214; Rv215; Rv217; Rv218; Rv219;
Rv21; Rv220; Rv221; Rv222; Rv223; Rv224; Rv225; Rv226; Rv227; Rv228;
Rv229; Rv22; Rv230; Rv231; Rv232; Rv233; Rv234; Rv235; Rv237; Rv240;
Rv241; Rv243; Rv244; Rv245; Rv246; Rv247; Rv249; Rv24; Rv251; Rv252;
Rv253; Rv254; Rv255; Rv257; Rv258; Rv259; Rv25; Rv260; Rv261; Rv262;
Rv263; Rv264; Rv265; Rv266; Rv267; Rv268; Rv269; Rv26; Rv270; Rv271;
Rv272; Rv273; Rv274; Rv275; Rv276; Rv277; Rv278; Rv279; Rv27; Rv280;

Rv281; Rv282; Rv283; Rv284; Rv285; Rv286; Rv287; Rv288; Rv289; Rv28;
 Rv290; Rv291; Rv292; Rv293; Rv294; Rv295; Rv296; Rv29; Rv2; Rv301;
 Rv302; Rv303; Rv304; Rv306; Rv307; Rv308; Rv309; Rv30; Rv310; Rv311;
 Rv312; Rv313; Rv314; Rv315; Rv316; Rv317; Rv318; Rv319; Rv31; Rv32;
 5 Rv322; Rv327; Rv328; Rv329; Rv32; Rv330; Rv331; Rv333; Rv334; Rv335;
 Rv336; Rv337; Rv338; Rv339; Rv33; Rv340; Rv341; Rv343; Rv344; Rv346;
 Rv347; Rv348; Rv349; Rv34; Rv350; Rv351; Rv352; Rv353; Rv354; Rv355;
 Rv356; Rv357; Rv358; Rv359; Rv35; Rv360; Rv361; Rv363; Rv364; Rv365;
 Rv366; Rv367; Rv368; Rv369; Rv36; Rv370; Rv371; Rv373; Rv374; Rv375;
 10 Rv376; Rv377; Rv378; Rv379; Rv37; Rv381; Rv382; Rv383; Rv384; Rv385;
 Rv386; Rv387; Rv388; Rv389; Rv38; Rv390; Rv391; Rv392; Rv393; Rv396;
 Rv39; Rv3; Rv40; Rv412; Rv413; Rv414; Rv415; Rv416; Rv417; Rv418; Rv419;
 Rv41; Rv42; Rv43; Rv44; Rv45; Rv46; Rv47; Rv48; Rv49; Rv4; Rv50; Rv51;
 Rv52; Rv53; Rv54; Rv55; Rv56; Rv57; Rv58; Rv59; Rv5; Rv60; Rv61; Rv62;
 15 Rv63; Rv64; Rv65; Rv66; Rv67; Rv68; Rv69; Rv6; Rv70; Rv71; Rv72; Rv73;
 Rv74; Rv75; Rv76; Rv77; Rv78; Rv79; Rv7; Rv80; Rv81; Rv82; Rv83; Rv84;
 Rv85; Rv86; Rv87; Rv88; Rv89; Rv8; Rv90; Rv91; Rv92; Rv94; Rv95; Rv96
 and Rv9.

24. The recombinant BAC vector of claim 22, which is selected from the
 20 group consisting of :
 Rv234; Rv351; Rv166; Rv35; Rv415; Rv404; Rv209; Rv272; Rv30; Rv228;
 Rv233; Rv38; Rv280; Rv177; Rv48; Rv374; Rv151; Rv238; Rv156; Rv92; Rv3;
 Rv403; Rv322; Rv243; Rv330; Rv285; Rv233; Rv219; Rv416; Rv67; Rv222;
 Rv149; Rv279; Rv87; Rv273; Rv266; Rv25; Rv136; Rv414; Rv13; Rv289; Rv60;
 25 Rv104; Rv5; Rv165; Rv215; Rv329; Rv240; Rv19; Rv74; Rv411; Rv167; Rv56;
 Rv80; Rv164; Rv59; Rv313; Rv265; Rv308; Rv220; Rv258; Rv339; Rv121;
 Rv419; Rv418; Rv45; Rv217; Rv134; Rv17; Rv103; Rv21; Rv22; Rv2; Rv270;
 Rv267; Rv174; Rv257; Rv44; Rv71; Rv7; Rv27; Rv191; Rv230; Rv128; Rv407;
 Rv106; Rv39; Rv255; Rv74; Rv355; Rv268; Rv58; Rv173; Rv264; Rv417;
 30 Rv401; Rv144; Rv302; Rv81; Rv163; Rv281; Rv221; Rv420; Rv175; Rv86;
 Rv412; Rv73; Rv269; Rv214; Rv287; Rv42 and Rv143.

25. A *Mycobacterium bovis* BCG strain Pasteur genomic DNA library,
 wherein said genomic DNA library comprises recombinant bacterial artificial
 chromosome vectors.

26. A recombinant bacterial artificial chromosome (BAC) vector, which belongs to the genomic DNA library of claim 25.

27. A recombinant BAC vector according to claim 26, which is selected from the group consisting of :

5 X0001; X0002; X0003; X0004; X0006; X0007; X0008; X0009; X0010; X0012; X0013; X0014; X0015; X0016; X0017; X0018; X0019; X0020; X0021 and X0175.

28. A method for detecting a mycobacterial nucleic acid in a biological sample comprising the steps of :

- 10 a) contacting the recombinant BAC vector according to claim 22 or 26, or a purified polynucleotide according to claim 10 with the mycobacterial nucleic acid in the biological sample ; and
b) detecting a hybrid nucleic acid molecule formed between said recombinant BAC vector or said purified polynucleotide and the mycobacterial nucleic acid in
15 the biological sample.

29. The method of claim 28, further comprising before step a), making the mycobacterial nucleic acid in the biological sample available to a hybridization reaction.

30. A method for detecting mycobacterial nucleic acid in a biological sample comprising the steps of :

- 20 a) contacting a first polynucleotide according to claim 10 that has been immobilized onto a substrate with the mycobacterial nucleic acid in the biological sample ; and
b) contacting a hybrid nucleic acid molecule formed between said first
25 polynucleotide and the mycobacterial nucleic acid in the biological sample with a second, labeled polynucleotide according to claim 10, wherein said second polynucleotide and said first polynucleotide have non-overlapping sequences.

31. The method of claim 30, further comprising before step a), making the mycobacterial nucleic acid in the biological sample available to a hybridization
30 reaction.

32. The method of claim 30 or 31, further comprising before step b), removing the mycobacterial nucleic acid that is not hybridized with the immobilized first polynucleotide.

33. A method for detecting mycobacterial nucleic acid in a biological sample comprising the steps of :

- a) contacting the mycobacterial nucleic acid in the biological sample with a pair of purified polynucleotides according to claim 20 ;
- b) amplifying said mycobacterial nucleic acid ; and
- c) detecting the amplified mycobacterial nucleic acid.

5 34. The method of claim 33, further comprising before step a), making the mycobacterial nucleic acid in the biological sample available to a hybridization reaction.

35. A kit for detecting a mycobacterium in a biological sample comprising :

- 10 a) a recombinant BAC vector according to claim 22 or 26, or a purified polynucleotide according to claim 10 ; and
- b) reagents necessary to perform a nucleic acid hybridization reaction.

36. A kit for detecting a mycobacterium in a biological sample comprising :

- 15 a) a recombinant BAC vector according to claim 22 or 26, or a first polynucleotide according to claim 10 that is immobilized onto a substrate ;
- b) reagents necessary to perform a nucleic acid hybridization reaction ; and
- c) a second polynucleotide according to claim 10, wherein said second polynucleotide is radioactively or non-radioactively labeled, and wherein said
- 20 second polynucleotide and said first polynucleotide have non-overlapping sequences.

37. A kit for detecting a mycobacterium in a biological sample comprising :

- a) a pair of purified polynucleotides according to claim 20 ; and
- 25 b) reagents necessary to perform a nucleic acid amplification reaction.

38. A method for detecting the presence of a genomic DNA, a cDNA or a mRNA of a mycobacterium in a biological sample, comprising the steps of :

- a) contacting the biological sample with a plurality of BAC vectors according to claim 22 or 26, or purified polynucleotides according to claim 10 that are
- 30 immobilized on a substrate ; and
- b) detecting the hybrid complexes formed.

39. A kit for detecting a genomic DNA, a cDNA or a mRNA of a mycobacterium in a biological sample, comprising :

- a) a substrate on which a plurality of BAC vectors according to claim 22 or 26, or
- 35 purified polynucleotides according to claim 10 have been immobilized.

40. A method for detecting a polynucleotide of mycobacterial origin in a biological sample, said method comprising :

- a) aligning at least one polynucleotide contained in a recombinant BAC vector according to claim 22 or 26 on the surface of a substrate ;
- 5 b) contacting the polynucleotide in the biological sample with the substrate on which the polynucleotide of step a) has been aligned ; and
- c) detecting a hybrid nucleic acid molecule formed between the polynucleotide in the biological sample and the aligned polynucleotide of step a).

41. A kit for detecting a polynucleotide of mycobacterial origin in a biological sample, comprising :

- a) a substrate on which at least one polynucleotide contained in a recombinant BAC vector according to claim 22 or 26 has been aligned.

42. The method of claim 9, wherein the procedure by which the polynucleotide contained in a clone of a BAC DNA library is prepared, further comprises amplifying the polynucleotide insert.

43. The method of claim 9, wherein the procedure by which the polynucleotide contained in a clone of a BAC DNA library is prepared, further comprises digesting the polynucleotide insert with at least one restriction endonuclease.

44. The method of claim 42, further comprising digesting the amplified polynucleotide insert with at least one restriction endonuclease.

45. The Polynucleotide of claim 16, wherein the mycobacterium strain is *Mycobacterium tuberculosis*.

46. The method of claim 33, wherein the amplified mycobacterial DNA is detected by gel electrophoresis or with a labeled polynucleotide according to claim 10.

47. The kit of claim 37, further comprising a polynucleotide according to claim 10.

48. The kit of claim 39, further comprising reagents necessary to perform a hybridization reaction.

49. A method for physically mapping a polynucleotide of mycobacterial origin in a biological sample, said method comprising:

- a) aligning at least one polynucleotide contained in a recombinant BAC vector according to claim 22 or 26 on the surface of a substrate;

- b) contacting the polynucleotide in the biological sample with the substrate on which the polynucleotide of step a) has been aligned under hybridizing conditions; and
 - c) detecting the location of the hybridized polynucleotide from the biological
- 5 sample.

50. The kit of claim 41, further comprising reagents necessary for labeling DNA and reagents necessary for performing a hybridization reaction.

CCTTCTACGCCCCGCGATCTCGCCGGAACCGTTGTGCTGGTGGGTGTTCCNACGCCCCGACATGCGCCTGGACATGCCGC
TGGTCNACTTCTTCTCTCACGG (SEQ ID NO. 458)

.....Rv349T7.seq:.....
TCGACGGTTTGGCGGCCTTAAATGCACTGAGGTCGTCAATTGACCCACAGCGGAAATGCCGACTATTGCGAGGCCTC
CTTCGCCTTGGCTGCCGAGAGGGGCTCCGCGGGAACCGCATGCAGGTATATGACCTCGGTTTCTCGGGTGCTACCGC
GTGCCTTGTNTANGATNANCTCGGCGTTGGAATTGTCCAGCCGCGCCAATTCATCGAGCGCANATTCTGACACNTGGC
CGGCGGCACATACGCTTACCCGTGGATCTGCTCCACAGGACCGCCCTGTCCGGATCCTGCTCACGGGTAANGGAAC
TTACGTGGCACTCGG (SEQ ID NO. 459)

Clone Rv34

.....Rv34SP6.seq:.....
GACCACGCCAGGCTAATCACGTGACGCTACCGAATACCTNCCTAGTGGTGCAGGCTCCCGCTGGAAATGGCCCTGTA
CCAACTCGCGCACCGGTGCCAG (SEQ ID NO. 460)

.....Rv34T7.seq:.....
CGGCACCCGACCCCTTTGAGCCGTCCGCCGTGGCCGCGGTGGAACCTGGCCGACGAGGGACTGATCGTGCTGGGCAAAT
TGGTCGATGGCACGCTGGCCGCCGATCTGAAGGTCN (SEQ ID NO. 461)

Clone Rv350

.....Rv350SP6.seq:.....
CTCAAGCTTGCCGTTACCCGACTTCCGGAGGGACACCATGAGCACCGCCAGCCGAGCACGAGGGCCAAACTCCGCCGA
CGCAGCGCGTTGGACTTGTGCTGGACAAGGGGTTAGCCGCCGAAGCAGTGACGTACATCGGCGAAAAGCAGTT
CGCCTGTGCGACCGACGGNGCNACCGTGAGGCTAGGGAAGCGAGGACACATGGCCGCCGACCGCAATGTACACGCT
GCAAGCAAACCATCGAACC CGGATGGCTATNCNTCACCGCCCATCGCCGCGGT (SEQ ID NO. 462)

.....Rv350T7.seq:.....
CATGTGCGGCACATCCAGGACTTCTGGGGGGATCCGCTGACAGCGGCGGGATCCCAAAGTGCGGATGATCGGGCCGCC
TACGTCGTGGTGTAACCTCGGTAAACAAGAAACCGAAGCGTATGACTCGGTCCACGCGGTGCGGCACATGGTGGAC
ACCACACCGCCACCGCACGGGGTGAAGGCCTATGTACCCGTCGCGCAGCACTCAATGCCGACAGGCGGAGGCCGA
GACAAAAGTATCGCTAAGGTCACCGCGATCACGAGCATGGTGATCGCAGCAATG (SEQ ID NO. 463)

Clone Rv351

.....Rv351SP6.seq:.....
ATACTCAAGCTTCGGTACGGTGGCGGGCGGTGCTGCTGGCCGCGGTGCGGGCGTGGCGGGCTGCGGTCTCGTTTACN
AGCTCGCGCTGCTGACACTGGCGGCNAGCCTGAACGGCGGCGGGATCGTGGCCACCTCCCTGATCGTCGCGGGCTACA
TAGCCGCGCTGGGAGCAGGCGCCTTGCTGATCAAGCCGCTACTTGACACGCGGCCATCGCGTTCATCGCCGTGGAGG
CGGTGCTGGGCATCATCGGCG (SEQ ID NO. 464)

.....Rv351T7.seq:.....
TGTCAGTCCTTTCAGATCTCNTTTTATGACATGACTGGAGATCTGTCTAGATTGCAGCTCCTGTGAGCGTGGGTAC
CGGATTCAAGCCGGTCGGTCACGCCGCGGTGGTACCGGCTTTGCGGCAGTGCTCGGCCTCGAGTTCGGCGATCGCGCG
CGAAGTGCGTTGCGCGAGCAAGATCGCGGCCGTAATGCCGCGGATGACCGCGATGACCAGCGCGATCCAGGAGAACCG
TTCCAACCACTGCTGGGCGGCCATCCCGGCGAAGTAGACCAGTGCACTGGTGCC (SEQ ID NO. 465)

Clone Rv352

.....Rv352SP6.seq:.....
CAATACTCAAGCTTCAAACAGGCCTGTTGTGGGCGCAACCGGCTCGCCGAGTTCTGCACGCACCGCCTCAANTGCGG
CCCGCACCGCCGGCATCTCCCGGTACGCAGGGCCGCGGCCCGCGCCGANCAGCGNGTGTTCCGCGCAGTTTCGCCGT
CAATGATGCTGACCTGATCGGCCACCCGGGCGTTCTCGGCGTCTCNCGTTCACTAATCGCGGTGCTC
(SEQ ID NO. 466)

.....Rv352T7.seq:.....
TACGTGGCGCTGGAGGGAGCCANNTACAACATCCACGCCAATGCTCTTGCCCCGATCGCGGCGACCCAGGATGACCCA
GGACATCCTGCCGCCCCAAGTACTGGAAAAGCTCACACCCGAGTTTCGTGCGACCGGTGGTGGCTACCTGTGCACCGA
GGAGTGTGCCGACAACGCATCGGTGTACGTGCTCGGTGGTGGCAAGGTGCAGCGAGTTGCGCTGTTTGGCAACGACGG
CGCCAACCTCGACAAACCGCGTCGGTACAAGATGTTGCGGCGCGGTGGGCGGAGATCACCGATCTGTCCGGTGCGAA
AATTGCTG (SEQ ID NO. 467)

Clone Rv353

.....Rv353SP6.seq.....
GCTTTTCCCGTCCGTCNNCGCTCAACCGCGTGAGGCCGAAGCGGNTGGTTACGACTCCCTGTTTGTGATGGACCACTT
CTACCAACTGCCCATGTTGGGGACNCCCGACCGCCGATGCTGGAGGCCCTACACGGCCCTTGGTGCGCTGGCCACGGC
GACCGANCGGTGCNNNTGGGCGCGTTGGTGACCGGCAATACCTACCGCAGCCCGACCCCTGCTGGCAAANATCATCAC
CACGCTCGACGTGTTAGCGCCGTCGAGCGATCCTCGGCATTGGAGCCGGTGGTTTGANCTGGAACA

(SEQ ID NO. 468)

.....Rv353T7.seq.....
CNGCTTTTAAATGGCCTTGACNTGGGCGNGCCGGCCACCGGGGCCACTCCGCACAATCTGTACCCGACCAAGATCTAC
ACCATCGAATACGACGGCGTCGCGGACTTTCCGCGGTACCCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCCGGC
ACCTACTACGTGCACTCCAATACTTTCATCCTGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTC
GGTCCCACGATGACCCAGTACTACATCATTGCGACGGAGAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATC
GTGGGAACCCACTGGCGAACCTGGTTCAACCAAACCTGAAGGTGATTGTAACTGGGCTACGGCGACCCGGCCTAT
G (SEQ ID NO. 469)

Clone Rv354

.....Rv354SP6.seq.....
CTCAAGCTTGCCGGGAGGGTGCATGGCCGACTCGGATTTACCCACCANGGGGCGCCAACGCGGTGTCCGCGCCGTCNA
GCTGAACGTTGCTGCCCGCTGGGAGAACCTGGCGCTGCTGCGCACCCCTGGTGGGCGCCATCGGCACCTTCGAGGACCT
GGATTTGCAGCCCGTGGCGGACCTGAGGTTGGCGGTGGACGAGGTGTGCACCCGGTTGATTGCTCGCTCGGCCTTGCCGGA
TGCCACCCCTGCGCCTGGTGGTGCATCCGCGAAANACGAANTTGTGGTGGAGGCTTCTGCTGCCTGCGACACCCACNA
CGTGGTGGCACCGGGCAGCTTAGCTGGCAT (SEQ ID NO. 470)

.....Rv354T7.seq.....
CCGACGCCGTCGTGGCCACCAACACCGCGACCGAGCACCGTGACCCGGACCGGGGTGCCGCGGAACCGGTCTTGGCCA
ATTGCCGCGGCACCAAGCCGTCGCGGCCATGGCGAACAGCACGCGGCATTGCCCGAGCATCAACACCATCACCACCG
TGGTAAGCCCGGCCAGCGCGCCGACGGAGATGATGCCGCTGGCCAGTACACCCCGTTGGCCTGGAACCGCGGTGGCCA
GATTTGCCGGCCCGCGGCCCGGTACGGTCCGAGTTGGGTGTATGGAACCATGCCCGACAGCACCCG

(SEQ ID NO. 471)

Clone Rv355

.....Rv355SP6.seq.....
TTNACTGGCCTTTGGTCCACACTAGACAATACTCAAGCTTCCAGGACATCGTCATCGCGACCAAAACCGCGAGCTAGG
TCGGCATCCGGGAAGCATCGCGACACCGTGGCGCCGACGCGCGCTGCCGGCAGGCCGATTAGGCGGGCAAATTAGCCC
GCCGCGGCTCCCGCTCCGANTACGGCGCCCCGAATGGCGTCACCGGCTGGTAACACGCTTGCGCGCCTGGGCGGGC
GCCTGCCGGATCAGGTGGTAAATGCCGACA (SEQ ID NO. 472)

.....Rv355T7.seq.....
NGACGCTTCCATCCGCGCGTCGTTTTGGCGGGTTGGCCACAGCAGCCCGCCGGTGACGGCGACGATGCTGGGCTGGT
TGCGGCCCTGCGCCACCGCGGCTTGCTGCTGGTTGGCTGTCTTGGGACGATCCCGAAATAGTCCACGCGGATCTGGT
GATTTTGGGGCTACCCCGGATTACCCGCGCGGCTCGACGAGTTTTTGGCCTGGACTACCCGCTGGCCAATCTGCT
GAACGCGCGCGGTGGTGGCCTGGAATGTCGAGCGCGGTACCTA (SEQ ID NO. 473)

Clone Rv356

.....Rv356SP6.seq.....
CTTCTCTGAGTACCNCCGTTACTTTGGGATGGGTAAAAAGGCGAATCNCCTTTGGTCACGAACGCCGGGAGGG
ACAACTCTCGGGCGGCTGGGGCCTCTCGCGGAANGCCCGAATGTACGGTGTCTCGACACTTCCNTCCCCCTCCG
(SEQ ID NO. 474)

.....Rv356T7.seq.....
GAGCATCGGGACNTACGGAGTCAACTACCCGGCCAACGGTGATTTCTTGGCCGCCGCTGACGGCGCGAACGACGCCNG
CGACCACATTGACGAGATGGCCAGCGCGTGCCGGGCCACGAGGTTGGTGTCTCGCGGCTACTCCAGGGTGCGGCCNT
GATCNACATCGTCACCGCCGACCACTGCCCGGCTCGGGTTACGCGAGCGGTTGCCGCCNCAGCGGACGATCACNT
CGCCGCGATCGCC (SEQ ID NO. 475)

Clone Rv357

.....Rv357SP6.seq.....
TACTCATGANCATCCTTTAATCANNGCTTTGCGTTTTTTATTAAATCTTGCAATTTACTGCAAAGCAACAACAAAT
CGCAAAGTCATCAAAAACCGCAAAGTTGTTTAAATAAGAGCANCACCTACAAAAGGAGATAAGAAGAGCACATACCT

CAGTCACTTATTATCACTAGCGCTCGCCGAGCCGTGTAACCGAGCATAGCGAGCGAACTGGCGAGGAAGCAAAGAAG
AACTGTTCTGTGAGATAGCTCTTACGCNCA (SEQ ID NO. 476)

Clone Rv358

.....Rv358SP6.seq:.....
CTCAAGCTTCAGGTCAATGTGCNCCAAGCCCTGACGCTGGCCGACCAGGCCACCGCCGCCGGANACNCTGCCAAGGCC
ACCGAATACAACAACGCCGCCGAGGCGTTGCGANCCCACTGGTGACCGCCGAGCANANCGTCAAAAACCTCAAGACG
CTGCATGACCAGGCGCTTANCCCGCANCTCAGGCCAAGAAGGCCGTCNAACGAAATGCGATGGTGCTGCACCANAAG
ATCGCCGAGCGAACCAAGCTGCTCAGCCNG (SEQ ID NO. 477)

.....Rv358T7.seq:.....
CATGGTGGCACTGTAGCGACGTGCTGCAATCAAGGTCATGCCGACTCTGGTCAGCTCGGANCCGCTGACACCCCGCT
AAGGCTGCTCAGCTCGGTGCATTACCTCACCGACGGCGAACTCCCCAGCTTTACGACTATCCGGATGACGGCACCTG
GTTGCGGGCGAAGTTTATCATCAGCTTGGACGGCGGCGCTACCGTCGATGGCACCAGCGGGCGATGGCCGGGCCCGG
CGACCGATTTCGTCTTCAACCTGTTGCGTGAAGTTGCCGACGTCATCGTGGTCGGCGTGGGCACCGTGCAGCATTGAGGG
CTACTCCGGCGTCCGGATGGGTGTCGTCCAGCGCCAGCAC (SEQ ID NO. 478)

Clone Rv359

.....Rv359SP6.seq:.....
TACTCAAGCTTGCGGGTGATCGCCTTGGTCAACGGCACCGTGATCGGATCGGGGTCNACCGCACAAATGGACTGGAGC
TTCGGCGAANTCATCGCCTATGCCTCGCGGGGGTGACGCTGACCCCGGTGACNTGTTGCGCTCGGGCACGGTGCCC
ACCTGCACGCTCGTCTATCACCTCNGGCCACCGGAATCATTCCCGGGCTGG (SEQ ID NO. 479)

.....Rv359T7.seq:.....
GTTGGNGCCTCGTCGGCGAACAGTTCTCGCACGATTTCCGGATTAGCGGGACTGGTCACCAGTTGGGTATGCGGGGAAG
GCGCTGACGTTTCGCCGCGATTAGCTGTTTGATGGACGCGGTGGTGATGTTCTGATCACGGAAGTGGCTGTAATAGCCC
AGGGTCGCCACGCTTTCATCCGGGCCCGGACCGGGCGACCGAGCGTGTCGCGCAGGTATGCGACGTGATTTTCGCTG
AAGTCCCCGTACCCGGAGAACT (SEQ ID NO. 480)

Clone Rv35

.....Rv35SP6.seq:.....
TGCTTCCGGCTCGTATGTTGTGTGGAATTGTGANCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACG
CCAAGTATTTAGGTGACACTATAGAATACTCAAGCTCCAGGTCAATGTGCGCCAAGCCCTGACGCTGGCCGACCAGG
CCACCGCCGCCGAGACGCTGCCTTTGTACCCGAATAACAACGCCGCCGAGGCGTTTCGACGCCAGCTGGTGACCG
CCGAGCAGAGCGTCGAAGACCTCAAGACGCTGCATGACCAGGCGCTTAGCGCCGACGCTCAGGCCAAGAATGCCGTCG
AACGAAATGCGATGGTGTCGCGGCATAAGATCGCCGAGCGAACAAGCTGCTCAGCCAGCTCGAGCAGGCGAAGATGC
ACGAGCA (SEQ ID NO. 481)

.....Rv35T7.seq:.....
CAGGCATGCAAGCTTCGGAGGCGAGCCCGTGATGGTGGCACTGTAGCGACGTGCTGCAATCAAGGTCATGCCCGACT
CTGGTCAGCTCGGAGCCGCTGACACCCCGCTAAGGCTGCTCAGCTCGGTGCATTACCTCACCGACGGCGAACTCCCC
AGCTTTACGACTATCCGGATGACGGCACCTGGTTGCGGGCGAACTTCATCAGCAGCTTGGACGGCGGCGCTACCGTCG
ATGGCACCAGCGGGGCGATGGCCGGGCCCGGCGACCGATTTCGTTCAACCTGTTGCGTGAAGTTGCCGACGTCATCG
TGGTCGGCGTGGGCACCGTGCGCATTGAAGGCTACTCCGGCGTCCGGATGGGTGTCGTCCATCGCCA
(SEQ ID NO. 482)

Clone Rv360

.....Rv360SP6.seq:.....
TACTCAAGCTTGGGGTGGCGCTGTGCGTGGTGCTTGGCGGCGTCGGTATCAACACCGCCACGAAATGGGGCACA
AGAAGGATTTCGTGGAGCGGTGGCTGTCCAAAATCACCTCGCCANACCTGCTACGGGCACTTCTACATCGAGCACA
ACCGTGGCCATCAGTCCGGGTGTCCACACCGGAGGACCGGGCGTCGGCGCGGTTCCGGCNAACGTTGTGGGANTTCC
TGCCCCGCANTGTTATCGGCGGCTTGCCT (SEQ ID NO. 483)

.....Rv360T7.seq:.....
GGCCATCGCCACCGCNC CGCGGCGAACGCTCAAAGGCACCTACTGGCACCAAGGCCCCACACGTCACCCCTGTGACCTC
CTGCGCCGACCCGCCCGAGGTCTTGGCCGTTACCACCGAACGGGCGAGCCGGGAGTCTGGTACGCATCGAACAAGA
GCAAGGTGCATGGGCGGAGTTGTTCCGCCACTTCGTCGATGACGGGGTCGATCCATTGAGGTCCGTCGCCGCGTCGG
TCGAGTGGCGGTCACTCCANGTACTCGACCTCACAGACGAGAGGACTCGATCCCATCTAGGTGTGGACGAAACAGA
TCTTCTGTCCGACGACTACACCACCCAGGCCATCGC (SEQ ID NO. 484)

Clone Rv361

.....Rv361SP6.seq.....
GCTTGC GGGTGATCGCCTTGGTCAACGGCACCGTGATCGGATCGGGGTCNACCGCNCAGATGGACTGGANCTTCGGCG
AANTCNTCGCCTATGCCTCGCGGGGGGTGACCTGACCCCGGGTGACNTGTTCCGGCTCGGGCACGGTGGCCACCTGCA
CGCTCGTCAAGCACCTCNGGCCACCGGAATCATTCCCGGGCTGGCTGCACNACGGCGACNTGGTCNCCCTCCAGGTG
AAGGGCTGGGCNAAACAANGCAGACCGTCCGGACAANCGGCACTCCTTTCCGTTGGCTCTTCGGCCGAATCCGGACG
CCNAACCCGACCGGCG (SEQ ID NO. 485)

.....Rv361T7.seq.....
GTTCTCGCACGATTTCCGGATTAGCGGGACTGGTCACCACTGGGTATGCGGGAAGGCGTGACGTTCCGCCGATT
GCTGTTTTGATGGACGCGGTGGTGATGTNCTGATCACGGAAGTGGCTGTAATANCCAGGGTCGCCNCGCTTTCATCCG
GGCCCGGACCCGGCGCACCGAGCGTGTGCGCGAGGTATGCGACGTGATTTTCGCTGAAGTCCCGGTACCCGGAGAACT
CGAACACGCTGAGGCGCTCGTCACCGTCGTNNCGGCGACCAAGCGCGGAGCAACTGCGCAAAATCGTTAAGANAGG
TCGAATCGTTGAAATTCCGGACCACTGCACC (SEQ ID NO. 486)

Clone Rv363

.....Rv363SP6.seq.....
CACAAACAATACTCAAGCTTCAGGTCAATGTGCNCCAAGCCCTGACGCTGGCCGACCAGGCCACCGCCCGCGGANAC
GCTGCCAAGGCCACCGAATAACAACGCCCGCGAGGCGTTGCGAGCCAGCTGGTGACCGCCGAGCANANCGTCNAA
AACCTCAAGACGCTGCATGACCAGGCGTTANCGCCNCAGCTCAGGCCAAGAAGGCGTCGAACGAAATGCGATGGTG
CTGCAGCANAANATCGCCGANCAACCAAGCTGCTCAGCCAGCTCGAGCAG (SEQ ID NO. 487)

.....Rv363T7.seq.....
CCACCCGTGCATGGTGGCACTGTAGCGACGTGCTGCAATCAAGGTGATGCCCGACTCTGGTCAGCTCGGAGCCGCTGA
CACCCCGCTAAGGCTGCTCAGCTCGGTGCATTACCTCACCGACGGCGAACTCCCCAGCTTTACGACTATCCGGATGA
CGGCACCTGGTTGCGGGCGAACTTCATCAGCAGCTTGGACGGCGGCGCTACCGTCGATGGCACCAGCGGGGCGATGGC
CGGGCCCGGCGACCGATTCTGTTCAACCTGTTGCGTGAACCTTGCC (SEQ ID NO. 488)

Clone Rv364

.....Rv364SP6.seq.....
GCTTTCCGCCGATACCCNCCATGTCCCGCACATCCAGGACTTCTGGGGGGATCCGCTGACAGCGGCGGGATCCCAAAG
TGCGGATGATCGGGCCGCTACGTCGTGGTGACCTCGNCGGTAACAACGAAACCGAANCGTATGACTCNGTCCACGC
GGTG (SEQ ID NO. 489)

.....Rv364T7.seq.....
CAACCCGANTTGGCTTTCGGCGCCNTCGGTGAGGACGGCGTGCGGGTGCTCAACGACGACGTCGTCGCGGGACACAC
CTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGATCTACNACGCCGNGNGGAACGCTTCNGCCCG
GGGCGTGACCGCNTCCCGTT (SEQ ID NO. 490)

Clone Rv365

.....Rv365SP6.seq.....
GGGATGGGCAAAAAGGCGAAGCACCGCGTGGCCACGAACGCCGGGAGGGACAATCTCGGGCGGCTAGGGCTTCTCGCG
GGAAGGCCCGAAGCTACGGCGTTTCAACACGTGCGCTCGCCCTCCGACCGCGAACATTCGGGGATGGCAGCAACCTGG
TAGCACCTGGCCGGGCGATGATCTGCCAGCGTCCCGCGGGTAGTCGCCGCCCGGGCGG (SEQ ID NO. 491)

.....Rv365T7.seq.....
CAGCAGACCAACAAGAGCATCGGGACATACGGAGTCAACTACCCGGCCAACGGTGATTTCTTGCCCGCGCTGACGGC
GCGAACGACGCCAGCGACCACTCAGCAGATGGCCAGCGCGTGCCGGGCCACGAGGTTGGTGCTCGGCGGCTACTCC
CACGGTT (SEQ ID NO. 492)

Clone Rv366

.....Rv366SP6.seq.....
CTCAAGCTTGACTGGCCACCCACCGGCATGACCACCGACAGGCCCGACTGGTTCGTACCACTCGAACGCCGGGGTGTTT
GA (SEQ ID NO. 493)

.....Rv366T7.seq.....
TTGGTGCCCGGAATGGCGAGTCCCATTTANTCGCTGATTTGTTTGAACAGCGACGAAACCGGTGTTGAAAATGTGCGC
TGGGTGCGGGATTCCCTCTCCAAGCAAGAGTAAGTGGCCCCAAATAAAGTTACTCGTCGTCTTGCAAAGACCGCTACC

CGATGCCATTTATGTGTTTCCTTACGCTCNNNNNTCCGGTGCGCCATCATTATCTGCACCTTTGCACTGCACATTGAG
CTTAGCAGCGCTCG (SEQ ID NO. 494)

Clone Rv367

.....Rv367T7.seq:.....
GAATTNGCTTTTCGGCGCCATCGGCCAGGACCGCGTGCGGGTGCTCAACGACGACGTGCTCCGCGGGACACACCTCGA
TGCTGCCGCCATGGACGCGGTGGAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGGAACGCTTCCGCCGCGGGCG
TGACCGCATCCCGTTGACCGGGCGGATCGCNGTGATCGTGCATGACGGCATCGCCACCGGAGCGACGGCCAAGGCGGC
GTGCCAGGTGCGCCGGGCGCACGGTGCGGACAAGGTGGTGCTGGCGGTCCCGATCGGCCAGACGACATCGTGGCGAG
ATTCGCCGGGTACGCCGATGAAGTGGTGT (SEQ ID NO. 495)

Clone Rv368

.....Rv368SP6.seq:.....
TAAAGCTTTCGTGAGTTTCATNGNCCCCCGGACCAACAAAAGCATCGGGACATACGGAGTCAACTACCCGGCCAACGG
TGATTTCTTGGCCGCGCTGACGGCGCNAACGACGCCAGCGACCACATTCAGCAGATGGCCAGCGCGTGCCGGGCCAC
GAGGTTGGTGCTCGGCGGCTACTCCCAGGGTGCGGCCGTGATCNACATCGTCACCGCCGCACTACTGCCCGGCTCGG
GTTACGCGACCGGTTGCCGCCCGAGCGGACGATCACNTCGCCGCGATCGCCCTGTTCCGGGAATCCCTCGGGCCGCGC
TGCGGGGCTGATGAGCGCCCTGACCCCTCAATTCCGGGTCCAANACCATCNACCTCTGCAACACGGCGACCCGATTG
TTCGGACGGCAACCGGTGGCGANCGCACCT (SEQ ID NO. 496)

.....Rv368T7.seq:.....
CCGGGAGGGACCATCNCGGCGGCTNCGGCTTCTCTCCGGAAGGTTCTANNGTNNNGCGTTTCNACNCTTCCCGTCGC
CCTGCGACCGCGGAACATTCGGGGTATGGNNGCANCTGTNAGCATCCNGGCCGGG (SEQ ID NO. 497)

Clone Rv369

.....Rv369SP6.seq:.....
CTCAAGCTTCCGCATCAGATCGCTATAGAACC GGTCGCGCTCCCCACCGAGTGGCTGGTCGCCTTCCAGCACGATCGT
TACCGGTTATCGGAATCAAACCTCNCGAACACCTGACCAACGCGCTTGATCGCCTGAATCGATGCGGCGTCGCTGGG
GCTCATCGATACCGAGTGTGCTTTTCCGACCACTTCCAGTTGCGGTACGGCGAGATTGACAAAGGCGGTGAAGCCAG
CCAGAGCAGGACGATCACCNCCGAAACCGGCGGATTTGCCCG (SEQ ID NO. 498)

.....Rv369T7.seq:.....
GCTTGGCAGCCTGCGGCTGGGCGCCCTNGAGCTCTTCGATCTGGATCTCCGACTCGAGATGCTCACTTGCCCCGGCCG
TGGACGTACCCATTGCGGCCGGGACCCAGCGCCCGAGGTGACCAGCGAGTTGGGCTGCACGCTGACCGGCCGTCGG
GGTCGACGCCGGTAACGGTCAGCAGCTCCGANCTCANNCTGATCCCGACCGCAGCTGCCAATGCGCGGCTGGCAGCCG
ACGTGGATGTGCCGGGGCTAGATCGCGGGGACGAGCGAGACCGCGTCACCGACGGTCATCACCTTGCCGAGTTTNG
GCCTGCCCGAN (SEQ ID NO. 499)

Clone Rv36

.....Rv36SP6.seq:.....
GCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTNCACACAGGAAACAGCTATGACCATGATTACGC
CAAGCTATCTAGGTGACACTATAGAATACTCAAGCTTGAGCCATCGGGCTATCAGCTGGTTGATGTCCCG
(SEQ ID NO. 500)

.....Rv36T7.seq:.....
CAGGCATGCAAGCTTGTGCTCTATCACATCCGACCACCAACCGCCCGACGGCTCGGCAGAACGCCTCCGCATATGGGT
CGACGACGAGCGGGTCGGACTTCTGGGCTGCCAGCGCTCGCGCCGTCGCGACAAACAGCGCGGTGCAACCGACACTCC
TTGTGATGTCCACCTATCACCTTCGGTACGCACCCAATCGACCTACCGGGCTAGCTCAGCCCCGATCTTCCAGAGC
TCCGCCCG (SEQ ID NO. 501)

Clone Rv370

.....Rv370SP6.seq:.....
GCTTTTTGAGCGTCGCGCGGGGCGGCTTCCCCGGCAATTCTACTAGCGAGAAGTCTGGCCCGATACGGATCTGACCGA
AGTCGCTGCGGTGCAGCCACCTCATTTGGCGATGGCGCCGACNATGGCGCCTGGACCGATCTTGTGCCGCTTGCCGA
CGCGGACGCGGTAGGTGCTCAATTCCGGTCTACGCTTGGGCTTTGCGGACGGTCCCGACGCTGGTCGCGGTTG
(SEQ ID NO. 502)

.....Rv370T7.seq:.....
CGANCTGTTTCGACGGCTACCTGAATCACCCGATNCCACCGCCGCGGCGTTTCGACGCCGACAGCTGGTACCGCACCG
GCGACGTCGCGGTGGTCGACGGCAGTGGGATGCACCGCATCGTGGGACGCGAGTCGGTCGACTTGATCAAGTCGGGTG
GATACCGGGTCGGCGCCGGTGAAATTGAAACGGTGCTGCTCGGGCATCCGGACGTGGCGGAGGCGGCAGTCGTGGGG
T (SEQ ID NO. 503)

Clone Rv371

.....Rv371SP6.seq:.....
NAAGCTTTGTACACCAAGTGTTCNACCAGNCGCTCCATCCGGCGAAGTGGATACTCCAGCAGGTAGCAGGTGCGC
ACCACGCTGGTCAGTGCGCTTCAGCTCGCTTGGCGGCTGCAGCAGCCAGTCCGGGAAATAGCTGCCCTGGCG

(SEQ ID NO. 504)

.....Rv371T7.seq:.....
CGCTGGNCGCCGGCGCTGGGCTGCGGTAACCAATTACCACAACACTTTTCGGTAGCCGAACAGCGGCGGTACCGCG
AAATGGCACAGCCACCGCAGTCGCGGACATCCGCGGAAGATGTGGCAGATTTTCGTGCGGTGAGCCGGCGAAGCCCT
AGCGTCATTGTTGCCTGGCAAGGTTGCTGGGCCCCG (SEQ ID NO. 505)

Clone Rv373

.....Rv373SP6.seq:.....
CTCAAGCTTCTTCTGCCCTTGGCGTTNCGGATNACATCCCGCAGCGACTCGGCTTCGGCGTCGATGTCGAAGTTCTC
GATCAGCTTCTGGATCGACTCCGCGCCATGGCAGCGTGAAGTACTCGCCGTAGCGGTGACNAGTTTCGGGTAGAG
GTTTTCGTTCNACNATCAGCTGCTTGGGCGCCANCTTGGTGAAAGTGCTCCAAATGTCCTCCAACCGGTCCAGCTCAGC
CTGCGCGCGGTACGGATCTGGCGCATCTCGCGCTCGCGCCGTTCGGAACCTGCGCCGCGCATCGGCCCTTGGGCCCC

(SEQ ID NO. 506)

.....Rv373T7.seq:.....
GTTACACCTACCTACTATGCCNCAATTCNCCGACAGGGTGGCATCAACACGGGCGATAAGGTGGAAATCGCTGGGG
TGAACGTCGGGCTGGTGCGCTCGCTGGCAATCCGCGGCAACCGCGTGTGATCGGATTCTCGTTGCCCGGCAAGACAA
TCGGGATGCAAGCCGGGCGAGCAATTCNCCNACACCATTCTTGGCCGTAAGAACCTGGAGATCGAACCCCGCGGTT
CGGAGCCGTTGAAACCAACGGTTTCTGCCGTGGCGCANACCACTACGCCATACCAATC (SEQ ID NO. 507)

Clone Rv374

.....Rv374SP6.seq:.....
CTCAAGCTTTACGCCGACGCCGCTACACAACACCAAGGAAACGATTGCCTACTGCCGAATCGGGGAACGGTCTCTCG
CACACCTGGTTGCTGTTGCGGAATTACTCGGACACCAAAACGTCAAGAACTACGACGGCAGTTGGACAGAATACGGC
TCCCTGGTGGGCGCCCCGATCGAGTTGGGAAGCTGATATGTGCTCTGGACCC (SEQ ID NO. 508)

.....Rv374T7.seq:.....
TCCNCATGGGATAACGGTTTAGATTTNACAACGGCACCGTGTTTCTCAACAAGCCGGTCATCAGCTGGGCCGGCG
ACAACGGTATCTACTTCACCCGCTTCGCCCCGTACAAGAAAAACCACTAGGCCACCATCGAGTCCAAGAACCAACC
TGGTCCGCAAGTACGCGTTCTACTACCGCTATGACACCGCCGAGGAACGCGCCGTGCTCAACCGGATGTGGAAGCTGG
TCAACGACCGCTCAACTACCTACCCCGACCATCAACCGATC (SEQ ID NO. 509)

Clone Rv375

.....Rv375SP6.seq:.....
CTCAAGCTTGGGTGTTGCCGATCACCGGAAGCCNATGATCAGCCACGTTTCGCGCCGCCCGGCATACGGCGGCGTAC
CGATCTCCGCGTCATACACCCGCGGTAATCGCCGACGGTGCCGGTTTCGCGAGCCGAAGGTGACAACGCTGATTGAAT
CNAGTTCANGTCCAGCGGT (SEQ ID NO. 510)

.....Rv375T7.seq:.....
TNAACAGCTCGCGGCAGCCACGACCTGCTGCGTCGGATTGCCGGCGGCGAGATCAATTCCAGGCAGCTCCCGGACAA
TGCGGCTCTGCTGGCCGCAACGAANGACTCGAGGTCAACCCGGTGCCCGGGGTCGTGGTGACCTGCCGATCGCACA
GGTTGGCCCAACAACCGGCGCTTGATGNNNGTCGGCAAGCCCGGCAGTNGCCAAACCCAGCGTGATCANGCTCGGCT
CGCGAGTTCGGCGAANAAGTGGCTCGCTGATCACCTACCATCGGCCANGATCTGCGTGTCA (SEQ ID NO. 511)

Clone Rv376

.....Rv376SP6.seq:.....
GCCANCCGGCTTGGCGTCGACTCCCGTTCNGCACATCATACGGTCCCCGGTACTGTCCAACGCGCCGGTGGCGTAGC
CAAACGTACGACTCTCAGTGATCCAGTTCGTGATCCGGCCGGTGGCGCCGCTGCGGCGGGGGCTNATNTACTTCGG
ACTNATTATCTCATCAAAGGACACCGGGCCGGTGGCTGGAATCCCATGGTGGGATCGGCCACACAN
(SEQ ID NO. 512)

.....Rv376T7.seq:.....
CCGACCTGGTATCTTCCGATAGCGCGCTTGATATCCGGTCTGATCTCCTGCCCTTAACGCCGGATCTCAGCAGGTCC
CCATGCAAAGATCCGAGGTGTCCNGATCTAGGGGTCTCGTCTCCAGATGATGGAGCAAGTCGGCCC
(SEQ ID NO. 513)

Clone Rv377

.....Rv377SP6.seq:.....
CTCAAGCTTCGGCTCAGGCGCGCTGCCGGTAACGTGCGTGACCGGTGCAGGTTTCGACAATGTGGTGCCGGTTCGGC
GGCTACGTGCCATCAAGACACTGGCGCAGGCTATCGCACCCGTTATCGGCTACAAACAAATCGCGGTATGC
(SEQ ID NO. 514)

.....Rv377T7.seq:.....
CATCACCTGHTTCATGAACGGAAGCACCGCAGCGCTTCCTTTTCGGCCGCAACATGAGCCAGCCTCTCGTCGGCGGT
CGGGTGCAGGTGCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCCTGAAACCAGCTTCCATATCCCGCGACGAACGA
CGCCAGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACAGCGCGTTCTCCACCGACCGGGCCCGGTGTGGG
GTGT (SEQ ID NO. 515)

Clone Rv378

.....Rv378SP6.seq:.....
AGCTTAGCTTCCCGCCCCGCAATAGGGCTCCAGCTCATCCGGTGTGACCAGATAGGGGCCCAGGGTGATACCGCTGT
CTTTGCCCTTGGCCTGTCCGATGCGCAGCTGGCCCTCCAGCATCTGCAGTCCCGTGGCGACCGATCGTTGAAAATGG
TATAGCCGATGATCGACCG (SEQ ID NO. 516)

.....Rv378T7.seq:.....
CCNGAACAGAAGCGGNGGTTCTACCGCGGTGTGCGGCCGGCGCGATATCGGCCTTTTACTAACCGAACCCGATGTG
GGCTCCGATCCGGCGCGCATGGCATCGACGGCGACGCCGATCGATGACCGCCAGGCTTACCACCTT
(SEQ ID NO. 517)

Clone Rv379

.....Rv379SP6.seq:.....
CTCAAGCTTGC CGGACTCGACAAGCATTCTTGACAGTTGTTTTGGCTCGGCATGGTTAGCCAAGGTTCTGCGGTCCCA
CCAGATCATCTTGGTCCGGTAGCGCTCGTCCGGGTATGCTGCCGCCGGGATTCTCGCTGCTATTACTCCCCCGAAGA
ACGCCACCGGTCCAGCGC (SEQ ID NO. 518)

.....Rv379T7.seq:.....
GCNAGGCGGTATAGCTTCCCGTGTACCGGCGACCGCCAGCCGAGAAGCTCGTTTTCCAGTGTTGCTGGGGATTCTC
ACGCTGCTGCTGAGTGCGTGCCAGACCGCTTCCGCTTCGGGTACAAACGAGCCGCGGGGCTACGATCGTGCGACGCTG
AAGTTGGTGTCTCCATGGACTTGGGGATGT (SEQ ID NO. 519)

Clone Rv37

.....Rv37SP6.seq:.....
GTGTGGAACCGTGAGCGGATAACAATTTACACAGGAAACAGCTNTGACCTTGATTACGCCAAGCTATTTAGGTGAGG
CTATATTAATACTCAAGATTGCGGTGAGCACATCGGCCCAAGAACCGCCGAAGGCACGGCGGAACGCCTGCGGCACA
TGGGGCGACGACGACGGGTGCGACTTCTGGGCTGTCCAGCCGATCGCGCCGTCGCGA (SEQ ID NO. 520)

.....Rv37T7.seq:.....
CACTGTCACTACATATGCGCCGCTCCTCCTCATCGCTGCGCTCGGCATCGTCGCCGGCGGTGATGGCGTCACCCTACC
CAAGCCGAACGCGAAGACGAGAACGTGTTCCATTATTAGGGTGTGAGCACCAATACCAGATTGCTCACCAGGAACCTCAC
GCAGCACCGGGACGGATGTGAGCCACCACGCCCATCTGGGGTGGTAGCGGGGAAATACGGCTAACGCGGCTCCGGTGC
CGGCAGCCCAGCGCAGACCCTCGGCGGGCGGACACGGCAACAACGACGACCCATAGTTGTTCTTTGCCGGATGGCCGT
GTTTGCGGACATATCGGGCGGGCGGCGGGCGCCGAGGTAGTGGCTGAGGCCCATCTCGTGCCCGCCGAATGGCC
CCAGCCAAACCGTGTA (SEQ ID NO. 521)

Clone Rv381

.....Rv381SP6.seq:.....
CTCAAGCTTTTACGGTGATCGCGCATCACCTGGTTCATGAACTGGAAGCAGCGCAGCGCTTCCTTTTCGGCCGCAACA
TGAGCCANCTCTCGTCGGCGGTGCGGTGCAGGTGCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCCTGAAACCAG
CTTCCATATCCCGCGACNAACGAC
(SEQ ID NO. 522)

.....Rv381T7.seq:.....
CTCAGAAGCCGCTAGCTGGTAGAGTCGCTGACCGGTGCACGTGGCGNCAATGTGCGCTGCCGGTTCGCG

(SEQ ID NO. 523)

Clone Rv382

.....Rv382SP6.seq:.....
CTCAAGCTTGCGCTCATCAAGCGGAACAGCAGGGCGGTGCGCTGGTGCCTATGACGGGTGACGGGACCAATGACGCA
CCCGCGCTCGCGCAAGCCGATGTCGGGGTGGCNATNAATACCGGCACCCAGGCGGGCCGGAAGCCGGCAACATGGTC
NATCTCCACTCC (SEQ ID NO. 524)

.....Rv382T7.seq:.....
ACTTCTATTTGACTGGTGTGCTGTGGCGGATCCGACTGCCGGCGTGGTCAAGGCCGGCCAGTTGTGGGATNCCACA
GGCAC
(SEQ ID NO. 525)

Clone Rv383

.....Rv383SP6.seq:.....
GCTTGTGCTATTCCGTGGCACTGTGAGACATATGCGCCGCTCCTCCTCATCGCTGCGCTCGGCATCGTCGCCGGCGGT
CATGGCGTCACCCTACCCAAGCCGAACGCGAAACGAGAAGCTGTTCATTATTAGGGTGTGAGACCAATACCAGATT
GCTCACCAGGAACCTCAC (SEQ ID NO. 526)

.....Rv383T7.seq:.....
CGATATTGCTCGGCCGCGTTGTCTGACTGGGTCGCGT (SEQ ID NO. 527)

Clone Rv384

.....Rv384SP6.seq:.....
GACCTCGGCCACCAAGCCGACGCGACCGTTCGAGGTGGCGATCCGGCTTGGCGTCGACCCGCGTAAGGCAGACCACAT
GGTCCGCGGCACGGCCANCTGCCACACGGCACTGGTAAGACTGCCCGCGTCGCGCN (SEQ ID NO. 528)

.....Rv384T7.seq:.....
CCGGAAGTCTAGGGGACGACCTACTCAGCGCAAATGTGCTAATGTGAGTCCGCCCCACCAGGGCAGATCAACCCAT
GTCGATGATGACCTACCCGGATACCGGATTGGCGGT (SEQ ID NO. 529)

Clone Rv385

.....Rv385SP6.seq:.....
AGCTTCAGTTCTCCACGACGCGTTCCCAAATGAATTTCCCGATCCCAATCTCGGTTGAGATACAGGTGCGCCATAC
CCCTTACTTCCGNAACGCTGGGCGGATTGGCCCTGCCGCTG (SEQ ID NO. 530)

.....Rv385T7.seq:.....
CCGCTACGGGTGCAACATGCATCCGAGACCGATGCTCGAGCGCGCACCCCACTCGCCGATGGCCGGAACCGGCTGG
TTACCCGGGTGGCGGCTGACC (SEQ ID NO. 531)

Clone Rv386

.....Rv386SP6.seq:.....
GCGGCTGGTTACGACTCCCTGTTGTGATGGACCACTTCTACCAACTGCCCATGTTGGGGACGCCCAGCAGCCGATG
CTGGAGGCCTACACGGCCCTTGGTGGCTGGCCACGGCGACCGAGCGGCTGCAACTGGGCGCNTTGGTNACCGGCAAT
ACCTACCGCAGCCCCGACCTGCTGGCAAAGATCATCACCACGCTCGACGTGGTTAGCGCCGGTCGAGCGATCCTCGGC
ATTGGAGCCGGTTGGTTTGGAGCTGGAACACCGCCAGCTCGGCTTCGAGTTCGGCACTTTCAGTGACCGGTTTAN

(SEQ ID NO. 532)

.....Rv386T7.seq:.....
GCCTTTCCGCACAATCTGTACCCAGGACCNTCTAAAAATCGAATACGACGGCGTGGCCGACTTTCCGCGGTACCCG
CTCAACTTTGTGTCGACCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAATACTTCACTCCTGACGCCGGAA
CAAATTGAGCGAGCGGTTCCGCTGACCANTNNTGTCGGTCCCACGATGACCCAGTACTACATCATTGCGACGGAGAAC

CTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGGTTCAACCAAACCTTGAAG
GTGATTGTAACTGG (SEQ ID NO. 533)

Clone Rv387

.....Rv387T7.seq:.....
GCAGACCAACAAGATGCATCGGGATCATACGCCGTCAACTACCCGGCCAACGGTGATTTCTTGGCCGCCGCCAC
(SEQ ID NO. 534)

Clone Rv388

.....Rv388SP6.seq:.....
CTCAAGCTTGCCAAAGAGACCTCGTCCACCAAGCNGGACGCGACCGTCNAGGTGGCGATCCGGCTTGGCGTCCACCCG
CGTAAGGCANACCANATGGTTCGCGGCACGGTCAACCTGCCACACGGCACTGGTAANACTGCCCCGCTCGCGGTATTC
GCGGTTGGTGAAAGGCCGATGCTGCCGTTGCCGCGGGGGCGGATGTTGTGCGGAGTGACAATCTGATCGANAGGATT
CAGGGCGGCTGGCTGGAATTCGATGCCGCGATCGCGACACCGGATCAGATGGCCAAAGTCGGTCNCATCGCTCGGGTG
CTGGGTC (SEQ ID NO. 535)

.....Rv388T7.seq:.....
CCACGGCGTGATCAAGGTACCGGCCGGGATGTTGCGCAATGGCAGGTTGTTGCCCGGCTTGATGTGCGCGTTAGCGC
CGGATTCACACATCCCTTGCGAAAGTCGTTGGGTGCAATGATGTAGCGCTTCTCCCATCGAGATAGTGGAGCA
ACGCAATCCGTGCGGTACGGTTCGGGTCNTACTCGATGTGCGCGACCTTGGCGTTGACACCATCTTTGTCAATTGCGGC
GAAAGTCGATCATCCGGTAAGCGCGCTTATGACCGCCGCTTTGTGCCGGGTGGTAATCCGGCCATGCGCGTTGCGTC
(SEQ ID NO. 536)

Clone Rv389

.....Rv389SP6.seq:.....
GGCGGCTGCGTGGCGAGATGATCGCCCGTGCCACCCGATCCGTGCCTCGGTGAGCGCCAACGTGCTTCCGGTCC
GGCGACCACCATGTCGCATGCGCCGAC (SEQ ID NO. 537)

.....Rv389T7.seq:.....
GCAATCGCCTTGGCGGTGCGCGGTTGTACCGGTGATCATCNGGNGCGGATGCTCATNCGGCGCATTTCGTCNAAT
CGTTCCCGTATGCCACCTTGACGATGTCTTCATATGGACCACGCCGATGGCCCNCGCGCTNCTG
(SEQ ID NO. 538)

Clone Rv38

.....Rv38SP6.seq:.....
CCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACGCCAAG
CTATTTAGGTGACACTATAGAATACTCAAGCTTCCACATCGGTATGCCAAAGCATTGCGCCGCTATCGATTTGCGGCT
GGCATCGCAAGGTGGACTTCTTGTCTAGCGACGAGATCCCGTGGTCCGATCCGCGGCTGCGCGGGCTGCGACCCGTG
CATCTCGGCGGCACCCGTGACCAGATGGCGCGCGCCGAGGCAGACGTGCGGCGGGGACGCCACGCCGACTGGCCGATG
GTGCTGGCCGCGTGTCCGACGTGCGCGACCCCGCCGATCGACGAAACCGGCCGCGCTCGGTTCTGGACCTATGCC
CACGTGCCGTGCGGGTCCACGCTCGACGCGACCGAGACCGT (SEQ ID NO. 539)

.....Rv38T7.seq:.....
CGCGTCCACCGCAGCGTGAGATTGGTGGCGCCATTTCGTGCTGGTGTAGCTGCTGTTGGCGGCGTCGCCGATTGTGCG
GGCCAGCCTTGTGCGGGGGCCGCTTCTACCCACGAGTCGGCACTTCCGCAACCGCCAGCTCGACCGCGATTACGGCG
GCCGAACGGCCGCCGAAGGCGTCTCGCAAGCGCCTTATCCTTTCGAGGTTCCAGATCCTTCCGCTACGTGGGTC
GCTCATCGCGGGGGCCGCGCAATGAGTACAGGTGAGGGTAACCGCTACAAATGAAGTTGGTCAGTGCTGGCCAACTG
TGTAATGGTTGCCCGGCTCGGGTACCACGTACATTCTGGCAAGGCGGGCGAGATTGGGTTCCGCGCTCCTTGGCCG
GTGGCGGTTCCCGGTTGTCCGTGGGCGTGTGCTGTACGTGGTGTAAAGTGTGCTGAACCTCCTCAGTTTGGGCT
(SEQ ID NO. 540)

Clone Rv390

.....Rv390SP6.seq:.....
CTCAAGCTTGCGCTGGATCTGGCGGCTGAGCCTGTTCTTGGGCAACATGCCGAGGGATCGCCTTTTCCACCACGCGGT
CGGGGTGGCGTTGCATTAGCTCACCGATGGTGCGCTTGTGAGGGCCCGGGATACCCCGAGTGCCGGTAAACCATCT
TGTGCTGCAGTTTGTGCGCGCTGATGGCGACCTTGTGCGCGTTGATCAGTATGACNAAGTACCGCCATCGACATTGG
GGCGAAGCTCGGCTTGTGCTTGC CGCGCAGCAGGTTGGCCGCCGCGACGGCAAGGCGGCCAANACCACGTC
(SEQ ID NO. 541)

.....Rv390T7.seq:.....
TTTGGGATGGGCAAAAGGCGAAGCNCCGCGTGGCCACGAACGCCGGGAGGGACAATCTCGGGCGGCTAGGGCTTCTC
GCGGGAAGGCCCCGAACGTACGGCGTTTCAACACGTGCGCTCGCCCTCCGACCGCGAACATTTCGGGGATGGCAGCAACC
TGGTAGCACCTGGCCGGGCGATGATCTGCAGCGTGCCTCGGGTAGTCGCCCGCCGGGCGGCTACAGTCTGAAACGC
GATGACCATCGATGTGTGGATGCAGCATCCGACGCAACGGTTCCTACACGGCGATATGTTCCGCTCGCTGCGCCGGTG
GACCGGTGGGTCTATCCCGGA (SEQ ID NO. 542)

Clone Rv391

.....Rv391SP6.seq:.....
CTCAAGCTTCGTCATAAGACCATGGTGCCTTTCTTTACCCGTCCANAGTCGGGGGCATCCGCACCGGCTCGCATCG
CATCATCTCCACGACGGGCGCTCATCAGCTTGGGCCATTTCAATGTACTTGATACCCCGCGTGGGGTAGGCCA
CTGCNACAATTCAAACACGGTGTACACGGTGAATANTGTGNANATGGGCTCTGATCAACCGTCNCAAACCGGTTTC
(SEQ ID NO. 543)

.....Rv391T7.seq:.....
GAATTCTGCGTGACCGCTATGGGTTGCAGCAGCGGCTGGCGCCGCACACCCCACTGGCCCGGGTGTTCGCCCCGA
ACCCGGATCATGGTGAGCGAAAAGGAGATTTCGCTGTTGATGCTGGGATTGCCACCGCGAGGCCATCGACCGATTA
CTCGCCACCGGGGTGCGAGAGGTGCCGAGTCCCGCTCCGTGACGTCTCCGACGATCCATCCGGCTTCGCCCGTCGG
GTGGCGGTAGCCGTGATGAAATCGTGCCTGCCGCGCTACCAACAGGTGATTCTGTCCCGTTGTGTCGAAGTGCCTTTC
GCGATCGACTTTCGTTGACCTACCGGCTGGGGCGTCTGCACAACACCCCGGTGAGGTGCTTTTGTGTCAGTTGGGC
GGAATCCGTGCTCTGGGTTACAGCCCCGAACCTCGTCNCGGCGGTGCGCGC (SEQ ID NO. 544)

Clone Rv392

.....Rv392SP6.seq:.....
GCAGTTGGGAATCGCTCTGCAGCAAACCANTATTCTGCGCGACGTTTCGAGAGGACTNNTTGAATGGACGGATCTACCT
GCCGCGCAGCAGCTGGACCGATTAGGCGTACNCTCCGCTGGACGACTCCGGGGCACTCGATGACCCCGACGGACG
GCTCGCGGCACTGCTGCGGTTTANTGCCNACCGCGCCGANACTGGTATTCGCTGGGACTGCGGCTGATTCCACACCT
CGACCGCCGCGAGCGCTGCCTGCTGTGCGGCCATGTCTGGCATCTACCGCCGTGNGCTCGCCTTGATCAGACCATCGCC
GGCGGTGCTCTACCATCGGCGAATCTCTGTTTCGGGACTGAANAANGCCCAAGTGGCGGCGGCGAGCACTGGNCTCTT
CGGTAACCTGCNGACCGCCCATTTGGACCGCTACCG (SEQ ID NO. 545)

.....Rv392T7.seq:.....
TTGATCTGGACGCTCTGAGACGGTGATCGGNCGAACCTGAATTGTCCGTAATGCCAGCGCAGAAAGCANGGTGGTG
GCCGGGGCGGTGAANCCGGCGTCGGCGGCACCGTCGAAGTCGATGTGGATTGCCGGAATGGGGATGTCCGGCACGGCG
AAGCCGTAGTTGCTTGTCCCGTGAGGCCANGTGGATGGGGGGAAGGATCGTGGTGTCCGGGATGATAATGGGGCCG
ATGCCGCGGTTGAAGTCCAGTGGATCGGGAATTCGGGAATCGTGATGCCGACGTTTCAGGCCGAACAGGCCCTCCAAG
TTGCCTCGCCACNAGATGCCGTTGCTGAAGTTGCCCGACATGAGGGCGCCGGTGTCCACATTGCCCGAATTGGCGACG
CCGGTGTGGC (SEQ ID NO. 546)

Clone Rv393

.....Rv393SP6.seq:.....
CACGTAGGCGCCGTCCATAAATNACTCCGCCGCGTTTCGCACATCCTCGTANCGATCCTTGGCGAGCAGGTCAACCGG
GCGCTGCCCGTCNAGGAGCCGGTTTTTGGCGTGACCCACTGGCCGACACCTCGGGGGGTAAAGCGAATCCGAGAGCAG
GAGGACNAGGTCACGAANCTGCGCCAGCCGGTCTGACCGCTCAGGGCGGATGTGCGCGGTCCGCCACCCCGGTACCGC
CCGATCGGACACCTGTATGACCGCGGCGACNTCGACCTGGGTGACGCCGAAGGTTTCAGGGCATCNACNATCTCGCT
GGCCTCGACCGCCCGGTCCAGGGTGACCGCCATCGTGTTTCTCCGCAACTTCGGGTTCTACTACCGTAAACGCTACC
G (SEQ ID NO. 547)

.....Rv393T7.seq:.....
CGGGGAACGGTCTCGCACACCTGGTTCGTGTTGCGGGAATTACTCGGACANCAAAACGTCAAGAACTACGACGGCAG
TNGGACAGAAACGGCTCCCTGGTGGGCGCCCCGATCGAGTTGGGAAGCTGATATGTGCTCTGGACCAAGCAAGGAC
TGACATTGCCGGCCAGCGTCGACCTGGAAAAAGAAACGGTGATCACCGCCGCGTAGTGGACGGTGACGGCCAGGCCG
TGGGCGGCGCGTTTCGTGCGGCTGCTGGGACNCTCCGACGAGTTACCGCCGGGAGGTGCTGGCGTCCGGCCACCGGG
CGAATTTCCGGTTCCTCGCCGCGCCCCGGGATCCTGGGACCGCNGGCGCGCGCTGTT (SEQ ID NO. 548)

Clone Rv396

.....Rv396SP6.seq:.....
CTCAAGCTTTGTCCGACAAGCGTTCCCGGGCGGTCAGCAAGCGAACGTGCGTTGGCCCACTGCGGGTCGATATTGCCG
CCAGGGA (SEQ ID NO. 549)
.....Rv396T7.seq:.....

CGTCAGCACGGCGACGTCGCGNTACGCCGAGCAGTTACACAATCGCTCTGCAGCAAACCAATATTCTGCGCGACGTTTC
GAGAGGACTTCTTGATTGGACTG

(SEQ ID NO. 550)

Clone Rv39

:Rv39SP6.seq:::

CTGCATCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTAC
GCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTCGCGCAGCGGGCGGTTGACCCGGTTCACGCCGTATAGC
TGGCCAATCTGGCATCGTCGATCANCATGTGGTGGGGGGTGACCTCGGCGGTGATCGAAATACCCTGGTCTTATCCC
ATTTACAGGATTTGACGGTGCCCGCGGCCGACGCGTGACAGATGTGACCCGGCGCGCGCTACCGGGCCAGCAAGG
CGTCGCGGGCGACGATCGATTCTCGGCGGCCCGCGGCCATCCCGCCAGGCCCGCGGCCATGGGTCCCTCGT
CGCGACGGCGCCGACCGTCAGCCGGGGCTCCTCGGCGTGCTGGGCGATCAGCACGCCCAAACCGGTG

(SEQ ID NO. 551)

:Rv39T7.seq:::

CCGACGCGCACTACGTGCTGGTGTCCACCCGCGACCCGCGACCGGCGACGAGCTACGCAGCTACCGCATCGTCGATGGCG
CTGTACCGAGGAACCTGTCAATGTCTGCGAGCAGTACTGAACCGTTCGAGAAAGGCCAGCATGAACGTACCCGTAT
CCATTCGACCATCTGCGGCCCCACACCGCGGCCGAGAAGTGTCTCGGCCAGCGCGCGCTACCTTGGGTGCGGTCA
TCAGCGACCTGGAGGCCAGCTATTCTGGGCATTTCGAGCGCCTGATGGACCCGTCTTCCCCAGGTAAGTTGCACCGCT
TCGTGAACATCTACGTCAACGACGAAGACGTGCGGTTCTCGGCGGCTTGGCCACCGCATCGCTGACGGTGACTCGG
TCACCATCTCCCCGCCGTGGCCGGTGGGTGAGCGGACACATGACACGATACGACTCACTGTTGCATGCCTTG

(SEQ ID NO. 552)

Clone Rv3

:Rv3SP6.seq:::

TGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACG
CCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGCCGGGAGGGTGCATGGCCGACTCGGATTTACCCACCAAG
GGGCGCCAACGCGGTGTCCGCGCCGTGAGCTGAACGTTGCTGCCCGCTGGAGAACCTGGCGTGTCTGCGCACCTG
GTCGGCGCCATCGGCACCTTCGAGGACCTGGATTTGACGCGCGTGGCCGACCTGAGGTTGGCGGTGGACGANGTGTGC
ACCCGTTGATTGCTCGGCTTGGCCGTGCGGATGCCACCTGCGCCTGGTGGTTCGATCCGCGAAAAGACGAAGTTGTGGTG
GAGGCTTCTGCTGCCTGCACACCCACGACGTGGTGGCACGGGCGAGCTTTAGCTGGCATTCT

(SEQ ID NO. 553)

:Rv3T7.seq:::

GGAAACACCGNCGCCGTCGTGGCCACCAACACCGCGACACGACCGTGACCCGGACCGGGGTGCCGCGGAACCGGTC
TTGGCCAATTGCCGCGGCCACCAAGCCGTGCGCGCCATGGCGAACAGCACGCGGCATTGCCCGAGCATCAACACCATC
ACCACCGTGGTAAGCCCGGCCAGCGCGCCGACGAGATGATGCCGTGGCCAGTACACCCCGTTGGCCTGGAACGCG
GTGGCCAGATTTGCCGGCCCGCGGCCGCTACGGTCCGCGATTGGGTGTATGGAACCATGCCCGACAGCACCCCGAT
ACCGCGACGTAGAGAAGGTCACGACCCCGAGCGACGCGAGAATCCCTCGAGGGACGTCTCGTTGAGGACGCTTGGTC
TCCTCGGCCATGGTGGCCACGATGTCAAACCCGATAAACGCGAAGAACACGATCGATGCCCGGCCAGCACGCCGTA

(SEQ ID NO. 554)

Clone Rv40

:Rv40SP6.seq:::

CCTGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTAC
CGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGTCTCGGGCGTGGCCTCGGCCAAGAAATCGTCGACGC
CGGCTCCTGTGCAATCGCCTTGGCGGTGCGCGGTTGTACCGGTGATCATCACGGTGCGGATGCTCATTCGGCGCA
TTTCGTGGAAGCGTTCCCGTATGCCACCTTGACGATGTCTTCAGATGGACGACGCCGATGGCCCGCGCGCTGCTGT
TATCGGTCCATTCCGCAACGACTAGGGGTGTCCCCCGCGGAGCTGATGCCGTGCAATGGCACCCACCTCCTCAG
TGGGGTGGCCACCGTGATCGAAAACCACTTCATACCGCAGCCGCGGCACCTTGGCGATCCGAACGGATGCGCTC

(SEQ ID NO. 555)

:Rv40T7.seq:::

TTCTGTCGATGGCGCGCCCGGCTACGGTTTGACCTGTGGGTGTGCAATTGGGGTCAAATTCGAGGTCGGCGCGCT
AAGAGTGGTCATCCTGCACCGCCCGGGGGCCGAACCTGCGCGGCTCACACCGCGCAACACCGACCGAGCTGCTGTGCA
CGGCTGCGCTGGGTATCCCGCGCGCATGACGAGCAGCAGCAATTCGCCGAGCTGCTGGCTTCCCGGGTGCGGAAGT
GCTGTTGCTGTGCGACCTGTTGACTGAGGCACTACATCACAGCGGGGCGCCCGCATGCAGGGGATCGCGCTGCCGT
CGACGCACCGCGGCTGGGACTGCCGTGGCGCAAGAACTTTCGGCTACCTGCGTATCTCGACCCAAGCANGTTGGCG
CATGTGCTGACCGCGCATGACTTCAACGAACCTCCNTCCGACACGCCGAACGAAGTGTGTTGGTGTGCGTATGC

(SEQ ID NO. 556)

Clone Rv412

:Rv412SP6.seq:::

GCGGCGAGTGTGGTGGGTGCCGAACACGAATCCAACGACGCACTGGCGGAGAGATACCACTTGCTGTACTGGAAGCAC
GTGCTGATGATCTCCCGTGAATGTGCTTGGCGCGCTCTATCGAAAACAGTGAGCATGCTGCG

(SEQ ID NO. 557)

.....Rv412T7.seq:.....
CAACCGCGCTCGGCGCGTCTGGGCTTCCGCCGGCTCCGCCGACAATTCTATCTCTGGATCAGCGGGGCTCTCCGGGC
CGGCTCCGCGAACTCAACAGGCGCGCTTCCGGCCGAAACATTCCCTAGCCATATATGATCGCACCTCGATACACG
ATCTGGCGGCAACACCGCAAAGCGTCCGACGGGCCAACCTCCGCAATTCAGGTATCCGGG (SEQ ID NO. 558)

Clone Rv413
.....Rv413SP6.seq:.....
GAAGGTCGGCGAAGGTGTGGCTGGNTGCCGATCACGAATCCAATGATGCAGTGGTCGGAAGATATTAGCCACTTGCTG
TTCTGGAGACAGGTGCTGATGATCTCCCGTGAATGTCCTCGACTCCGTCTATCGAAATCTGTGAACA
(SEQ ID NO. 559)

.....Rv413T7.seq:.....
TCCTGCGCTCTGGGCCATTCTCGGGTCTGCCGACAATTCTATCTCTGGATCTGTGGGGCTCTCTTGGCCGGCCTCNGC
GATCTCTTCANGGCGCGCTTCCGGCCGAAACATTCCCTATCCATATATGATCGCACCTCTATACACCGTTTGGCGGC
AACACCGCAAAGTGTCTGTCG (SEQ ID NO. 560)

Clone Rv414
.....Rv414SP6.seq:.....
AGCTTTACGCTGGCGTATCAGCGTTGGGGCCGCTGCCATTTCCGTCGCCCAACGCGTTGCCAGCTCCCTGCGCTGTCA
GGGCTTGCGCGCCAAACTGGCCACCGCAACAACTTGCTGAGCTTGATC (SEQ ID NO. 561)

.....Rv414T7.seq:.....
CTCTATCTGGCGTCACATTCGCAATCTTTAGATTGCAGATATCGATAAAATCACCCGCGCGACAAGACCGCCATGTCA
TCCTTTCGATGTTATTTGCCCGCTGGGGAAAGCGCAACGACGTTGCCTACACGTTCCGCGCT (SEQ ID NO. 562)

Clone Rv415
.....Rv415SP6.seq:.....
AGCTTNCCTTGCATCTGCACCCGATCCACGTCAGCCACGTCGGCGTTCTCCACCAAGAAGTTGCGGGCATTCTCCT
TGCCCTGGCCGAGCTGCTCGCCCTCGTAGGTGAACCAGGCACCCGACTTGCAGGATGAGGCCCTGATCCACACCCATGT
CGATCAGCGAGCCCTCCCTGCTGATTCCCTTGCCGTAGAGGATGTGCAACTCGGCCTGCTTGAAGGGGGGCGAACACT
TGTGCACGACAACCCCTTCGGCGACGAGGGTGTGCAGTTCTCGACCTCGAGGTCGAACGTTTCGTGCCCGCCGCGTTG
GCAGCACTTCTCGGATCACGGAATAGCGGANTTCTTCCGCCAGCATGTCTGTCAGGAATTTGTCTATCCAGGGCATCCG
CGAGCGCTGCACGCG (SEQ ID NO. 563)

.....Rv415T7.seq:.....
ACTGTCNAGGGAATGCTTCGCGAGCATCTACCTGCAGTCGCTTGTGCATAAGCGGACGGCCCNACCTGTTCTGTTCGG
GGACACCAGACGCGGGAGCACCGGCAGTACGGCGAAAGGTTTGAGCGGAAGGAGTTGCGCAAATCGGGGCGCCCCAAC
ACCCGTCCGCAAGACGCGGTCAACGACCTGTTTCAGGCGATCAGGGTCACCGACTCACCTGCACTGAGAACAAGCGAT
CTGCTGATCTGCCAGAAGATGGACATGAATGTCCACGGCAAGCCTGATGGCCTGCCGCTCTTCCGGGAATGTTTGGC
(SEQ ID NO. 564)

Clone Rv416
.....Rv416SP6.seq:.....
TGAATTATGATCCCACACAACCTGCATCANTTTAGCCGCTCGNGATGCTATCCGCCGACGTTTGGANCGGTCCGT
GTCGTTTCGTGTTGATCTCACCCGAAGTTGTGTCCGCCGCCGCCGGGATCTAGCGAACGTGGGATCGACAATCAGCGC
CGCCAACAAGGCGGCGAGCGGCTGCCACCACGCAGGTGCTGGCCGCGGGCGCCGATNAGGTGTCAGCGCGCATCGCGGC
GCTGTTTGGTATGTACGGCTGNAATATCCGGCGATCAGTGCGCAAGTTGCCGCGTATCACCANCAGTCCGTGCAG
(SEQ ID NO. 565)

.....Rv416T7.seq:.....
AACGGGGACCNAAGAAACATTCAANAACGAGGGTTCGTACCAACGTCGAAACCGACGGTTGCCAGCCGGCCACG
ATATTGCTGCTCGAGGGTCCGCTGTACCCTCACCGAACGTGAGTCCCACACCGCGGAGCGGGCGACTCTGGCGTGC
TTAGCAGCCGAGCTCAAGGTGTCCCGCAACTGTCTCGAATGCTTTTAAACCGACCGGATCAGCTCTCCGCCGATCTA
CGTGAACGAGTGCTTGCCACGGCCAAGCGACTGGGCTATGCCGGACCGGATCCGGTGGCGCGATCGTTGCGGACCCGC
AAAGCCGGTGCGGT (SEQ ID NO. 566)

Clone Rv417

.....Rv417SP6.seq:.....
AGCTTTGGAGCCNCNCCGANCCNCCGGTACGCCCCGCCACCGCCGTACCCGGCACCAGCCCTTTGAGCCGTTCCGCC
GTGGCCGCGGTGGANCTGGCCGACGAGGGACTGATCGTGCTGGGCAAAGTGGTCGATGGCAGCTGGCCGCCGATCTG
AAGGTCGGCATGGAGATGGAGCTGACGACCATGCCGCTGTTCCGCCACNACGACGGTGTGACGCGCATCGTCTACGCG
TGGCGGATCCCATCGCGCGCCGGCGACNATGCANAGCGCANCGATGCTGAGGAGCGGCGCCGATGAGGATGAGCGCGC
CGGAACCCGTTTACNTCCTGGGTGCCGTATGCACCCGTGGGGGAAATGGGGTAATGACTTC (SEQ ID NO. 567)

.....Rv417T7.seq:.....
TTCTCNCATCGTTCTACTNNGATGGGACGCTGCTGCCGAGGCGATCCTGGCCAACCGGCTCTCGCCGGCGCTGACC
TTGGCGGGGGCGAACCTGAACCTTCTTCCGATGGGCGCTTGGGCCAAACGTACCGGGGCTATCTTCATTGGCGTCAG
ACGAAAGATATTCCTGCTACCGCTTCGTATTACGTGCTTACGCCGCGCAGCTGGTGAAAACCATGTCAACCTCACC
TGGTCGATCGAAGGGGGTTCGGACCAAGACGGGCAAGCTACGGCCACCGGTGTTGGGGATCCTGCGTTACATCACCAGT
GCGGTCGACGAAATCGACGGTCCCAGAGTGTATTGGTGCCGACCTCGATCGTGTACGAACAGCTGCACGAAGTGGAA
GCCATGACCACCGAAGCCTATGGCGCCGTGAA (SEQ ID NO. 568)

Clone Rv418

.....Rv418SP6.seq:.....
TTCTTCCGGGTACCGCTGATCGGCGGCACCATCACGCACCCGGTGCAGGGCGAGGCGGCCGCCGGTGTGGTGTGCTA
CGGCCGGCCAGCCCGGTACCGGTGTGATCGCCGGTGGTGCGGCCCGCGCGGTGCTGGAATGTGCGGGGGTGCACGAC
ATCTTGGCCAAGTCGCTGGGCAAGTGAACGCGATCAATGTGGTGACGCCACCGTGGCCGCGCTCAAGCTGCTGCAC
CGTCCGGAGGAGGTGGCGGCGCGCGCGGTTTGCCAATAGAAGACGTCCCCCGGCCGGGATGCTG (SEQ ID NO. 569)

.....Rv418T7.seq:.....
GTCGAAAGTGACCATCTCTACCTTGAGTGCCATACCGCCCGACCCCTATGCCTCGGATAGCTCGGCGGAAAGAAACGCT
TGCAAGTGCAGCCGAATAGGCGGCTACGTGCTGAGCGCCCATCAACTCTCGCGCGGAGTGCATCGCCAGCTGGGCGGGC
CCGACGTGACCGTGGGGATTCCGGTGCGCGCCCGCGGCCAACGGCCCGATCGTTCGACCCGCACGGCAGATCGGCGCGA
TGTTCTGAACGCTGCATAGGCACTCCCGCGCGCTGGCAGGCAAGTTGCGAAACGCCCCCGCGGGTGCCTTCCGTGCG
TTGGCTTTACCGCAAATTTGGGGTTGCCCCCT (SEQ ID NO. 570)

Clone Rv419

.....Rv419SP6.seq:.....
AAAGCCACGGAAACGATTGCCTACTGCCGAATCGGGGAACGGTCCTCGCACACCTGGTTCTGTGCGGGAATTACTC
GGACACCAAACGTCAGAACTACGACGGCAGTTGGACAGAATACGGCTCCCTGGTGGGCGCCCCGATCGAGTTGGGA
AACTGATATGTCTCTGGACCAAGCAAGGACTGACATTGCCGGCCAGCGTCTACCTGGAAAAA (SEQ ID NO. 571)

.....Rv419T7.seq:.....
TTTCGCCACCGCNAGGTGCTGCGGTTCCAGAAAAGCGTGGTTTCGCCGGGCGCGAGGATTCGACGGTCCAACCTGACC
AGCCGGTCCCGCCACCCGTTAGGCAGGATCGCGGTGTCTATATGTTCCGCTCGGCATAAACGCCATTGCTGCGGTGA
AAATCGGACATCTCGCCGATTGCCACGTCTACATGATCCGCTTTGTCCCGCGCCGGGTCGTTGACAAACGCGATGTCN
GCCTCCTGGGAAGCGGTGGC (SEQ ID NO. 572)

Clone Rv41

.....Rv41SP6.seq:.....
TCGCCAAGTGGATTCTGTCTCACCNACGAGATCCGTGGTCCGATCCGCNGCTGCGGGGGGCTGCGACCCTGCATCTCG
GCGGCACCCGTGACCAAATGGCGCGCGCCGAAGCAGACGTCTCGGCGGGACGCCACGCCGACTGGCCGATGGTGTGG
CCGCGTGTCCGCNCGTCNCCGACCCCGGCCGATCNACCAAACGGCCGCCGTCCGTTCTGGACCTATCCACGTGCC
NTCGGGGTCCACGCTCGACGCGACCGANAACTAACCAGCGTCCTCGANCGGTTGCCCCCGGCTTCCGTGACATCGT
GGTGGCGGGCGCGCCGT (SEQ ID NO. 573)

.....Rv41T7.seq:.....
GTACCGTCACCATGATCGCCCCATCGGCATCGGTGAGCTGATAGATCCAGCCGGTTTCGCCAACCCTGGAGCGATC
TTGGCGCGCTGCTNGTNGTCNCTGANACNTAGCCACCAACAGAGCCCGGTGTGCGACAAGANGACTGATCGGATCTCT
CCGGACACNTCGAGGGGGTCTCAGGAGNCCGGCGCCACCCGAGGTAAGCCTCCGCCAGCCTCACACCGCGACCG
GGTATCNCAAGTCGCGCAATAANCCACCACCTCCTCGGACCCACGTTGTATGCGGCTGGGT (SEQ ID NO. 574)

Clone Rv42

.....Rv42SP6.seq:.....
ATACTCAAGCTTAGACCTCACTGATGTGGCGGGACGCGGGAGATAACCGCGGTTTCAGCCGTTCAACAGTGGTGGTTC
CCACACCACTTGTGCTTTGCGAAGTAAAGCGATTGATTTGCTCGAAAAGAGGGCTGGCTGCTCGTGAGGGACAT
CCATGGCCGATACCTCAGCGATCTCAACGGTCAAGCGACTGCATGTTGGCGCAAGGTATCGCTAAGCATAGGTTTCGT
GACGGATTGACAGCAAGAGCTTTCAAAGATTGCTGTCCACATANTGATTGCGATCTCTACACCTCTTCGCCGGTGC
TGTCAGAGCCATTGCAATCAGTTATCTCGCTCGTGCTTGGAAANAATTTCCAGCCTGCGTTGGACAAACCGCGTC
GCCAAGCGGT (SEQ ID NO. 575)

.....Rv42T7.seq:.....
AGCTTCCCGAGAAACAGTGCATTCCCTAAGCAGCCCGTTGTACGCGCGATGAGTGAAGAGTGCACGCAATCGCCGGAA
TCCGGCAAAGCCCTGCACAAGCGAAATCAACCCGAGGGCTGACAAAGGCAACGTCGGTGATCCGTACCGCTGGTTGGA
CAAACGGCAGAAGGCGGCCTCGTCCGGTCCATCTACGCCGAGCACACTGGTGATAGCGCGCATCGGCATCGGTGCGGC
CACGGTGGAGACGACGTCGCGGGCGTCTGGGTGAGTAACCCGCCGACAGTTCTCGGGCAAGCTGGTTCGACCATCGG
GCGCCACGTCCTCAACGCGCCACGCGCCATACCTGGTGCCAGTTGCTTGCATCCGGGTGTGCGCCGGCGGATCGGA
CGTCGAGAAACGCGACCCCGTGAGAGTGACCCACGGCGCTGGACACGTGTCTGGTTAC (SEQ ID NO. 576)

Clone Rv43

.....Rv43SP6.seq:.....
CGGCCGGGATGTGCGCAATGGCAGGTTGTGCGCCGGCTTGATGTGCGCGTTAGCGCCGGATTCCACCACATCCCCTTG
CGAAAGTCCGTTGGGTGCAATGATGTANCGCTTCTCCCATCGAGATAGTGGAGCAACGCAATCCGTGCGGTACGGTT
CGGGTCGTATCGATGTGCGCGACCTTGGCGTTGACACCATCTTGTGTCATGGCGGCGAAAGTCGATCATCCGGTAAGC
GCGCTTATGACCGCCGCTTTGTGCCNGGTGGTAATCCGGCCATGCGCGTTGCGTCCACCGCGACCGTGCAGCGGGCG
CACCAGCGACNTCTCCGGGGTTGACCGGGTGATCTCGCGCAAATCAGATACGCTGGCGCCGCGACGACCGCGCTCGT
GGGCTTGTAATTGCGAATTGCCATGGTCTAATCAGGTCTTCTCTCACCTCTCGTCGCCGGGCTAGGGCGCATGCGCT
GTCCT (SEQ ID NO. 577)

.....Rv43T7.seq:.....
TAGCGGTGTAACCAACTCCCGGGTACCACCCGCAAACCTCTGCGGCAACAGCACCGTCGACGCGTCAACCGGGCTG
CCCGGAATCCTGTGGATGGGCATCGAGTGCATGGTCACGACGTCCTCGACGCGCGCGGTGGCAACGACAAGTGGCCCG
GATGCACCACAAATGACGCGCGCACACCGGTGGGGACGGCCAGCACGAGAGCCGTGTGCGCGAAGTCGACGCTAATGC
CGTAGGCATTGGCCGTCAACACAGGCGACGCCCCGCGTACCACCGAGTCCACGGNGGTTGGGCGGTCTCCTCGGCCAA
CCAGGCGTGAACCCGGCGGATCCGAATGCAGCAAGACCCGTGGGC (SEQ ID NO. 578)

Clone Rv44

.....Rv44-2ndSP6.seq:.....
CCATTGGTCGGTGTGCGCATACCANTACNACGCGCGGGCACCTGACGCGGCGGCGCAACCATTCGGTGGCCATCGC
CATCGTCTGCCACCCGGTCAACGGACGCACCTTCTCTGGCCGACCTAGTGCGCCACCCGCGCGGTTGCGTCCCAT
CGATCCGCTCAACATGAGCAGCGCAAACCCGAGGTACATGACATCTGCTGTGGAACAGTGACANATTCGCCCGC
CCATGATGATCNTCGACCGTCCTCCGGATTGGTC (SEQ ID NO. 579)

.....Rv44-2ndT7.seq:.....
GCCGGCCTGGTCAAAGGGGCGTCCGAAGGANCCGGGCTGGGTAACAAGTTCTGGCTCATATCCGCGAATGCGACGCC
ATTTGTGAGGTGGTGGGGTGTTCGTGACGACNACGTGACTCATGTACCGGACGGGTGCGATCCCCAGTCCGACATT
GAGGTGCTGAGACCGAGCTGATCCTGGCAGATCTGCAAACCTGGAGCGGGCCACGGGCCGGTGGAGAANGAAGCN
CGACCAACAAGGCGCGCAAGCCGGTCTACGACCCGGC (SEQ ID NO. 580)

Clone Rv45

.....Rv45SP6.seq:.....
GATCCACTGACCACGATGACATATCGAAATGCTCGACGATTCCGATGGCGATCAAGGCCACGATGCCCTGGCGGTTGG
GCGGTATCTGGTGGATGGTGTACCCGCGGTAGGTTCCCGTGATCGTGTGACCCAGTCCACGCGATGGGCGGCGAGGT
CGTCGGCACGATACCCCCGCGTNTGCCGCCGAGTGCGCCTCGAGTTTGGCGGCCAGCTCTCCCCGGTAGAACTCTC
ACCGTTGGTCGCCGCGATCTTCTTANCGTCGCCGCGTGGTCAGGAAAGGTAACAGCTACCGGGTTTCGGCGCTCG
TCCGCCGGGCATGAACGCATCTGCGAATCCGGGCTGGGATGCGAACAACGGACCTGTGCCG (SEQ ID NO. 581)

.....Rv45T7.seq:.....
TCTACTGCCGAATCGGGGAACGGTCTCGCCACCNGGTTGCTGTTGCCGAATTACTCAGGACACCGAAACGTCGAG
AACTACGAGCGGAGTTGGACANAATACCGCTCCNNGTGGGCGCCCCATCGANTTGGGAAGCNGAAATGTGCTCTGG
ACCCACCCAAGAATGACATTGCCGGCCGCCCTCAACTGGAAATAGAAACNGTGATACCCGCGCGGTTCTTGAAG

GAATGGCATGCCCTGGGCCGGGCGTTCTTCCGCTGCCGGACTCCTCCCACCAATTCACCGCCGAAGGCGTCCCGTCT
GC (SEQ ID NO. 582)

Clone Rv46

.....Rv46SP6.seq:.....
ATACTCAAGCTTCTGTACCCGAAATCCCGCATGGGATAACGGGTTTAGATTTGACAAACGGGACCGTGTCTCAACA
AGCCGGTCATCAGCTGGGCCGGCGACAACGGTATCTACTTCACCCGCTTTCGCCCGT (SEQ ID NO. 583)

.....Rv46T7.seq:.....
CTGGCTCAAGCGCTCGGCCGCGCAGGTGAACCTCGGACCGGCTCGACGTCGCCGAACGCGAGGCGGTGCTGGCCACGCC
GACGCCGTCGTCGCACATATCGGCACCGTGCACAACTTACAACAACGCCGGCATCGCGTACAACGGCAACGTCGACA
AGTCGGAGTTCAAGGACATCGAGCGCATCATCGACGTCGACTTCTGGGCGCTCTCCACGGGCCC (SEQ ID NO. 584)

Clone Rv47

.....Rv47SP6.seq:.....
CCGCCCTCCGCATTATGGGTCAAGAACCATCGGGTCGGACTTCTGGGCTTCCAACGCTCGCGCCGTCCCN
(SEQ ID NO. 585)
.....Rv47T7.seq:.....
CCGTGGCACTGTGACACATATGCGCCGCTCCTCTCATCGCTGCGCTCGGCATCGTCGCCGGCGGTGCTGGCGTCACC
CTACCCAAGCCGAACGCGAAACGAGAACGTGTCCATTATTAGGGTGTGAGCACCAATACCAGATTGCTCACCAGGAA
CTCAGCGCAGCACCGGGACGGATGTGCGCCACCACGCCCATCTGGGGTGGTAGCGGGGAAATACCGCTAACCGCGGTCC
GGTGCCG (SEQ ID NO. 586)

Clone Rv48

.....Rv48SP6.seq:.....
TACTCAAGCTTGTCCAAATATCGAAGCGTCGGGTCGCGAGGCTCGGTCCGACAGCTCCAGCAAAACCCGCTCCACCCCT
AGATGCCGGTATCCCTCAAGGTCTTTATCCGCCGCTTCACCCCACTGGCACACGGTCACCGGCACGTGCCCCCGGCC
ATGGCCGCGCAACCGCTGAAGCGGACCCGACAGCCGCTGCGGTGATGGACTGATCGCGATCCACCCGGCATTGAGCCGG
GCTATCCGCGGGAAGTTCGCCGGTCCCCGCCCCACATACAGCGGAGGATAGGGCTTTGTACCGGCTTCGGCCAGCAG
TAGATCGGATCGAAGTCCACATATGTCCCATGGAATTCGCGCTGCTCCTGCGTTGAGATCTCGATTATCGCGCGCAAC
CGCTCATCGATCACACGTCCGCGCACCCGAGGGTCCACACCATGGTTGGCGACTTCTTCGCGCAACCAGCCACACCCA
CGCCGAAACGAAACCGTCCCTGCG (SEQ ID NO. 587)

.....Rv48T7.seq:.....
CAGGCATGCAAGCTTGGCCAACTCCTCATCGGACTTGAAGGTGCCGTCTCGTTGGCGGCCCTGCTCCACGGCACGTT
GATGGCACCAGGAATGTGTCCGGGCCGCTGGCTTTGTCTGCGGCAGGTGCGCGGGGGCCAGGATCTTGCCGGAGAA
CTCGTCGGGAGAGCGCACGTGATGAGGTTCTTGACGTTGATGGCCGCCAGGACCTCGTCGCGGAATGCCGAATCGT
GTTATCCGCGGGGGANGCGGTGTAGGAAGTCACCGGCCGGCTGACCGGTCGCTGGACAGCGGGCGTCCGTCGAGCTC
C (SEQ ID NO. 588)

Clone Rv49

.....Rv49SP6.seq:.....
ATACTCAAGCTTCAAAACAGGCCTGTTGTGGGCGCACCCGGCTCGCCGAGTTCTGCACGCACCGCCTCAAGTGCGGCC
CGCACCGCCGGCATCTCCCGGTCACGCAGGGCCGCGGCCCGCGCCGACGCGACGGCGTGTTCGCGCAGTTCGCCGTCA
ATGATGCTGACCTGATCGGCCACCCGGGCGGTCTCGCGCTCGTCCCGTTCACTAATCGCGGTGCTCAGCAGCGTCTCG
ACAGCCACCAACCGAGTGGAGACCAGATGCNCCACCACGGACCGCAGCGATGCCAGTCACCTCACCCGTCC
(SEQ ID NO. 589)

.....Rv49T7.seq:.....
CAGGCATGCAAGCTTTGCACTTGTGAGTAATGTGCGCCAACGTCACCACAATCGCGATGAATTCATATGCCGCCC
AGGGCGGCCAACCAATGGTGGCCGCGAGCGGCAGCTCGATCGCAGCGCGGAGGTTGCCGGCCGCGAGTTGATTACG
AACAGGGTGAGGTATAGCGGGCAGGATAGTGACGAAGGCAAGACCTAGATCTGCCGTGCGAAGAAGAATCGAGTAT
CCGGTCGACACAACGGAAGCGAAAGTGTCCGCGATGTTGATGAGCGTCGCCGGTTGTGGCGGCGGTGGCGGCGGTAGC
ACCGTCGCAATACCGCGGAACCGGGCATCCGAATTTGGGGCAGGGTGTCAAGGCGGCTGGCAACTCACCATGA
ATCT (SEQ ID NO. 590)

Clone Rv4

.....Rv4SP6.seq:.....
CCGGCTCGTATGTTGTGTGGAATTGTGACCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACGCCAAG
CTATTTAGGTGACACTATAGAATACTCAAGCTTGGCCCGCAGGGCCGAGTCGATTGGTCGCGGTCGCCCTCGACAGTTAG
CTTATGCAATGCTAACTTCGGGGCAAAGTTCAGGCGGATCGGCCGATGGCGGGCGTAGGTGAAGGAGACAGCGGAGGC
GTGGAGCGTGATGACATTGGCATGGTGGCCGCTTCCCCCGTCGCGTCTCGGGTAAATGGCAAGGTAGACGCTGACGTC
GTCGGTCGATTTGCCACCTGCTGCCGTGCCCTGGGCATCGCGGTTTACCAGCGTAAACGTCGCCCGGACCTGGCTGCC
GCCCCGTCTGGTTTCGCCGCGCTGACCCGCGTCGCCCATGACAGTGCGACCCTGNACCGGGCTGGCC

(SEQ ID NO. 591)

.....Rv4T7.seq:.....
GTGTGCTGTCAATTCAGAGCTGAGCCTGATGCACTCAACTTACTGAGCATGCTAACGCTGGTCGTGCGGGTCTTGTTCC
CCGCGTGTGCGCAGGGCACACGCTCGGGGCGTAGCTGGGAGAGGCCCCGGTCAAGCCCGGAGAGCAGTGCTCAGTCCG
CCAGCTTGACCGACTTTCGATGAGAACGCGCTTCTCGCCGTATTGAACTGGCGTGCTGACGGTCGCTGAGCAGCGCTC
GCCGAGTGCGGCCGCTGATTCTTTCATCGAGCCAGGAGGCGCATTGCTGTTGCGCCGCTGCGGGTCGCCCCCATCGT
CGACGCGATCCGTCACCCACTCCTCGATCAGGTCTGCCTCATCGAACGGGCCAACGGTGCTGTGCGAGTAAAGTGTCG
TGGGCACGCGAGCCGGTGCTGTGGTACACCCACCGTTGCATGAACAA

(SEQ ID NO. 592)

Clone Rv50

.....Rv50SP6.seq:.....
ATACTCAAGCTTCACCAGGCGCGCGGGCGCGGCCAAGCCAGGCAGCCGCGCTCGGCGCGTCGGGGCCTTCCGC
CGGCTCGGCCGACAGTTTCGATCTCTGGATCGGCGGGGCTCTCCGGCCGGCTCGGCGACCTCAGCGGGCCGCGCCTT
CCGGCCGAACCATTCCTAGCCATAGATAACCGCACCTCAATGCACGGTTTGCGCGCAACCCGG

(SEQ ID NO. 593)

.....Rv50T7.seq:.....
AGCTTCCGTCACGACCCGCCCTCGCCGCTGCCGGCGCCATCGGTTCATCGGATCTCATGACGACGTCACGTAGGCCCGC
TAGCCGCGAGCGGGCGCGGTCAACTGGCGAGGCGGGCGGACGTCAGTGAAGTGGCCGAGCTGGACCGGTTACCGCG
GAATAACCGTTCTCGCTCGACGACTTTCAGCAGCGGGCTGACGCGCGTGGAACGCGGCCACGGTGTTGCTGGTGTG
CGCGCCGACCGGCGCTGGCAAGACGGTGCTG

(SEQ ID NO. 594)

Clone Rv51

.....Rv51SP6.seq:.....
ATACTCAAGCTTGCCGGGACCGCGGAACAGAACCGGCGGTTCTACCGGGTGTCGGGCCGGCGGATATCGGCCTCC
CGACTAACCGAACCCGATGTGGGCTCC

(SEQ ID NO. 595)

.....Rv51T7.seq:.....
ACGTTGGCTCTGCCGGAACGTATTTCCAGCGGCACGCATTCCGGCGTGGGTGCCGGGCGCCGAGTTGCGTCGCTGGGAT
CACGCAGCAGTCGCCGGCGGCTGCCGTGCGGGCTATGAATTGCACCGAGCCGGAATCCNCAC

(SEQ ID NO. 596)

Clone Rv52

.....Rv52SP6.seq:.....
ATACTCAAGCTTGTCGTATTCCGTGGCACTGTCAGACATATGCGCCGCTCCTCCTCATCGCTGCGCTCGGCATCGTCG
CCGGCGGTTCATGGCGTCACCTACCCAAGCCGAACGCGAAACGAGAACGTGTCCATTATTAGGGTGTGAGCACCAAT
ACCAGATTGCTCACCAGGAACACGCAGCACCAGGACGGATGTCAGCCACCACCCCATCTGGGGTGGTAGCGGGGA

(SEQ ID NO. 597)

.....Rv52T7.seq:.....
CGTTGGTAGCCGATATGCATAGTGTATCTTACTGAACATGATTTCCATTATGGAGCCCGGGGTGCCGGCAGCGCGAA
CGGTGCGCCGTCAGACGCGGGCGGCACTGACCAGGTGTTGCGGGCGAACATCGGCCCGGCTTCGGATTCCGGTCCGG
GTACCGGGCGACCCACCGCTTCGAGGTA

(SEQ ID NO. 598)

Clone Rv53

.....Rv53SP6.seq:.....
ATACTCAAGCTTGGCCAACTCCTCATCGGACTTGAAGGTGCCGTCTCGTTGGCGGCCCTGCTCCACGGCACGTTGAT
GGCACCAGGAATGTGTCCGGGCGCTGGCTTTGTTCCTGCGGCAGGTGCGCGGGGGCCATGATCTTGCCGGAACACTC
GTCGGGAGAGCGCACGTCGATGAGGTTCTTGACGTTGATGGCCGCCAGGACCTCGTCGCGGAATGCCGAATCGTGTT
ATCCGGCGGGGAGGCGGTGTATGAGGTACCGGCCGGCTGACCGGGTCGCTGGACAGCGGGCGCTCCGTCCAGCTCCCA
CTTCTGCGGGCGCGTCCAACNACTTGACTTCTCCTGG

(SEQ ID NO. 599)

.....Rv53T7.seq:.....

ATATCTTAAGCGTCGGGTCCCGAGGCTCGGTCCGCGAGCTCCAGCAAAACCCGCTCCACCCCTAGATGCCGGTATCCCT
CAAGGTCTTTAGCCGCCGCTTCAACCCACTGGCACACGGTCACCGGCACGTCGCCCCCGGCCATGGCGCGCAACCGCT
GAAGCGGACCCGACAGCCGCTGCGGTGATGGACTGATCGCGATCCACCCGGCATTGAGCCGGGCTATCCGCGGGAAGT
TCGCCGGTCCCCCGCCACATACAGCGGAGGATAGGGCTTTGTACCGGCTTCGGCCAGCAGTAGATCGGATCGAAGT
CCACATATGTCCCATGGAATCCGCCTGCTCCTGCGTCCAGATCTCGATTATCGCGCGCAACCGCTCATCGATCACAC
GTCCGCGCACCGCAGGGTCCACACCATGGTTGGCGACTTCTTCGCGCA (SEQ ID NO. 600)

Clone Rv54

.....Rv54SP6.seq.....
ATACTCAAGCTTGTGCGGTAAACCCGCGAGCGGGCGGTGGGTGCGGTGTCAAAAACAACCACACTTCTTTGCGGTTC
GGTGATCTCGACACCGGCCGCGAGCCGACCATGCGCGCGTAAATCGGCGATCAGCGCGTCGGCTATCGCCTGGGT
GCCGCCACCGGAATCGGCCAGCCGACCGAATGGGCCAGCGTTGCCAGCATCAGTCCGGCGCCGCGCCGACACAGTGA
CGGCAACGGTGAAATCGCGTGGGCGGCAACGCCGTGAACAACGCGCGGGCATCTCGCCCGCCAGCGACCGCCAGGC
AGGGGTGCCCTGGGCCAGCATCCGCGAGCCCGAGACGCGAGGACCGAGCCAGTGCAGTAGGCAAAGACCGCTTGTGCGA
GACATGAAGTCCACGACCGT (SEQ ID NO. 601)

.....Rv54T7.seq.....
AGCTTATTGAACCGCGGGTCGCGAGGCAAAGTGGACCTCATAACGACTCGGGTCCAGCGACCGCGCCAACACGAACGGC
CGGACGAGCTGGGCCAGGGTCGCGGCCCTCCCTACAAACAGGATCCGTTGCCTGCGAGCGACAGGCTCCGGTGCGGCG
TTGGGCGCCGTGCTCGTCCAGCGTCCGGTCCCGGTGCGCGCGCAGCGTTGTTTCTCCATCTCGCCCCCTAATCT
CGAGGCAGCCCGTACCCGCGAGGCAACCTCCCAAAAATGCAATCCCCAAAATGCAATGCGTTCGAGCTATTTCTCACAC
CGACCGCTAGTTGCGGATCAGAAATCCGTTGGGCGCGGAAGTCCAGCCGAATTTGTTCTCCGCTCCGCATCATGCTT
GTAATCGTTTGAAATTCATCCTCATATGCTCGATCGCTTCATAGGGTCCAGGCCAAACCGGGCA

(SEQ ID NO. 602)

Clone Rv55

.....Rv55SP6.seq.....
CTTCCGGCTCGTATGTTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACGCC
AAGTATTTAGGTGACACTATAGAATACTCAAGCTTGGCCACCTCGCGGTGTGTGGTGGAAACCATCTGAGCAGTGTG
CCAAACCGGGGCGAGACAGCTCCCAATTGACGTGAGCCGCTCACTTGCTGGGTAAAGCGTCG (SEQ ID NO. 603)

.....Rv55T7.seq.....
TAGCGCCCCCTCCCGGGCGGAGCTCCACGGCGTGGATCAAGGTACCGGCCGGGATGTTGCGCAATGGCAGGTTGTTGC
CCGGCTTGATGTGCGCGTTAGCGCCGGATTCCACCACATCCCCTTGCAGAAAGTCCGTTGGGTGCAATGATGTAGCGCT
TCTCCCCATCGAGATAGTGGAGCAACGCAATCCGTGCGGTACGGTTCGGGTGCTACTCGATGTGCGCGACCTTGGCGT
TGACACCATCTTTGTCTATTGCGGCGAAAGTCGATCATCCGGTAAGCGCGCTTATGACCGCCGCTTTGTGCCGGGTGG
TAATCCGGCCATGCGCGTTGCGTCCACCGCGACCGTGCAGCGGGCGCACCGAGCGACTTCTCCGGGTTGACCGGGTGA
TCTCGGCGAAATCAGATACGCTGGCGCCGCGACGACCAAGCGTCTGCGGCTTGTCTTGCGAATTGCATGTCTAATCA
GGTCTTTCTC (SEQ ID NO. 604)

Clone Rv56

.....Rv56SP6.seq.....
TGAAACTATATAATACTCAAGCTTGCCAAAGAAGACCTCGTCGACCAAGCAGGACGCGACCGTCGAGGTGGCGATCCG
GCTTGGCGTCGACCCGCGTAAGGCAAACAGATGGTTGCGGGCACGGTCAACCTGCCACACGGCACTGGTAAGACTGC
CCGCGTCGCGGTATTGCGGGTGGTGAAAGGCCGATGCTGCCGTTGCCGCGGGGGCGGATGTTGTCGGGAGTGACGA
TCTGATCGAAAGGATTCAGGGCGGCTGGCTGGAATTCGATGCCGCGATCGCGACACCGGATCAGATGGCCAAAGTCGG
TCGCATCGCTCGGGTGTGGGTCCGCGCGGCTGATGCCCAACCCGAAACCGGACCGTCACCGCCGACGTCGCCAA
GGCCGTGCGGGACATCAAGGGCGGCAAGATCAACTTCCGGGTTGACAAAGCAGGCCAACCTGCCTTCTC

(SEQ ID NO. 605)

.....Rv56T7.seq.....
GCTGAGCTCCACGGCGTGGATCAAGGTACCGGCCGGGATGTTGCGCAATGGCAGGTTGTTGCCCGGCTTGATGTGCGC
GTTAGCGCCGGATTCCACCACATCCCCTTGCAGAAAGTCCGTTGGGTGCAATGATGTAGCGCTTCTCCCATCGAGATA
GTGGAGCAACGCAATCCGTGCGGTACGGTTCGGGTGCTACTCGATGTGCGCGACCTTGGCGTTGACACCATCTTGTC
ATTGCGGCGAAAGTCGATCATCCGGTAAGCGCGCTTATGACCGCCGCTTTGTGCCGGGTGGTAATCCGGCCATGCGC
GTTGCGTCCACCGCGACCGTGCAGCGGGCGCACCGAGCGACTTCTCCGGGTTGACCGGGTGATCTCGGCGAAATCAGA
TACGCTGGCGCCGCGACGACCGAGCGTCTGGGCTTGTAATTGCGAATTGCCATGTCTAATCAGGTCTTCTCT

(SEQ ID NO. 606)

Clone Rv57

.....Rv57SP6.seq:.....
ATACTCAAGCTTGTTGGTGACCTCGCCGGCGAACAGTTCTCGCACGATTCCGGATTAGCGGGACTGGTCACCAAGTTG
GGTATGCGGGAAGGCGCTGACGTTGCGCCGCGATTAGCTGTTTGATGGACGCGGCGGTGATGTCCTGATCACGGAACTG
GCTGTAATAGCCCAGGGTCGCCACGCTTCCATCCGGGCCCGGACCCGGC (SEQ ID NO. 607)

.....Rv57T7.seq:.....
GATGATCGCCGGTGCCACCCCGATCCGTGCCTCGGTGACGCGGAACGTGCTTCCGGTCCGGCGACCACCATGTGCGCA
CGCACCGACAGGCGCAACCCGCGGCCCGCACATGCCCGTTGATGGCGCCGACCACCGGCAGCGGCGACTCGACGAT
GGCGCGCAACAGCGCGTCAATTCGCGCGCCGCGCCACCGCCATCCGGTACGGATCACCACCACCTCCGCCGGCCCTC
GCTGAGGTCC (SEQ ID NO. 608)

Clone Rv58

.....Rv58SP6.seq:.....
ATACTCAAGCTTGCCGCAATCGAAACCAACCTGTTGTGCCGCAAGAAATTACGCCGTGGCCCGGCGCCGATCAAGAA
ACGCCCCGGCGCGCGGCGGTGTCGTGATGGCATGACGGGCACCAATGTGACGCCATTGTGAGCAGGCACCGGTG
CCAGCCCCGAATCCGGTGACACAGGCGACACCCGCGCCACACCCGGTATCGACGGCGCGCTGCTGTTGCGCGCTGTCG
GCCAGCTCGCAGGACGCGTGCAGCAACCCGCGCGCGGTGGCCGATTGGGTCT (SEQ ID NO. 609)

.....Rv58T7.seq:.....
TTGGCGGGTTGGCCACANCCCGCCGGTGACGGCGACGATGCTGGGCTGGTTGCGGCCCTGCGCCACCGCGGCTTG
CATGCTGGTTGGCTGCTTGGGACGATCCCGAAATAGTCCACGCGGATCTGGTGATTTTTCGGGGTACCCGCGATTAC
CCCGCGCGGCTCGACGAGTTTTCGCTGGACTACCCGCGTGGCCAATCTGCTGAACTCGCGGCCGGTGGTGGCCTGG
AATGTCCANCGCCGTTACCTACGTGACCTTGATGGGATCCGGGGGNT (SEQ ID NO. 610)

Clone Rv59

.....Rv59SP6.seq:.....
NCGTGGACACCGGTGTCGANCGCCACCAGCCGCATGTCTGCANGTCNATTCGGTCCTCGGCAACATCTTGAATGCCGA
GCAGCGCTGGGCGTGATCGGCAACCGGGGATGACCGCTCGCCGATCCGCTCGACAATCCCGGCGGCACGTGACATGC
CGGCGGACGGCTCGACGAGCTGGAACCTCAGCGACGACGATCCGGAATTGATCACCAGCAGGCTGCTACTCATGGACC
CCTGCGCCTGAATCCCGTGATGGCCACGGTGTGACTATTCTGTCGACAGTGACCCCGAGATAGTCTTACGGCTGCGT
(SEQ ID NO. 611)

.....Rv59T7.seq:.....
CATGTATTGCCGTGCTCACGGCGCCACGCTCGATGGTTTCTGAAGTCTCCGGGCTGGTGACAGCTTCTCGTTGATC
TCGTTGCCACGCGCTCCTCTCCCGCCGACGACCCGATCTCGATCTCCANAATGATCTTGGCGGCCCGCCGCGCTT
GAGCAGCTCCTGGGCGATGGCCAGGTTCTCATCGATGGGCACTGCCGACCGTCCACATGTGCGACGGAACAAAGATG
TCACCTTGCTCACGCGTGCCNAGATCNCANAAGGGCCGGACATACTGTNACTTGTCTTGGGCACTGGTCCGTGTC
AGCCACGTGACGGGTACTTGGCGCGATAACGTGGTG (SEQ ID NO. 612)

Clone Rv5

.....Rv5SP6.seq:.....
GCCACCACGACCCGGCGTAACCTGCTCACGGAATGCGGCCAGGCGCGCGTAGCACGTGGTATCCGCCATAAAGG
TGACCTTAAGCACGGCGTCCCAATTCTCGAACGACATCTTGTGGAAGGTGCCGTGCGCGAAGATCCCGGCGTTGCTC
ACCACACCGTGACGGCGCCGAATTCGTCAAGCGCGTCTTGATGATGTTGCTGCGCCGTCTCGGTGGCGAOGCTG
TCCTTAGTTGGCGACCGCCCGCCCCCTTGTGCGGAATCTCGGCGACGACCTCATCGGCCATCGCCGAACGGCGCCC
GTGCCCGTTCGCGGGCGCCACCGAGGTCGTTGACCACGA (SEQ ID NO. 613)

.....Rv5T7.seq:.....
CAGGCATGCAACCTTTGTCCACACGGCGTCTACTCCGTGCAAGGTCCGACCGCTTCCACGTCCCGCCGTGACGGTGCT
CCATCTCCCTCAGCAACGCGTGAAAGTGGTCCGATCCCGCGGCTTCAGG (SEQ ID NO. 614)

Clone Rv60

.....Rv60SP6.seq:.....
GTTGAGACGCAACCAGCGACAACGACGATTTGGCGTAGCGGGCGGACGTCTGCTCGATTTCGATCACGTGCGCTCGCA
TCGAGCATGGCCCGCGACGCTACACGATCGCCGTGCTGATGACACGACCGAGCCGTACGCCGGCGGTAAGCCGCGCC
AGGATTTCGGCGAAAAACGTCTACGTGGCGGGTGTACTGGGTGTGCAATGATTCTGTTGGGTGCGTATGCGTCTTCAAT
CGTCGACATAGATCCGTGCGCGCATCGCGTCGACAACTCCGGGTGAGTGGAAATACACTTGCCGATCACCGACGTGCG

CGGATCGATGCCGACCGAAATACGACCACATGGCTCTTGTGTCNCAGTGTGGCGGCATCAAATACCCTCAGTGCCGT
CCGAC (SEQ ID NO. 615)

.....Rv60T7.seq.....
TTNCCGCCTTNACGCCTACTCCNAGACGATGCTCGACGCGTGTGAGCACACGGCGCTGCTGTAGACGGCACGGCGCAG
CTGGATCGCGCTTGGTGCACCAAGCCTCTACGCGCGTGCCTGCGTCATCGGGTACCGAACATATTCCGGTCTGT
GCGCAGAGTGTGCATGTGCGGCTCTTGTGAACGAACATAGCAAAGCGTATATGTCTGTGGCGGCTCTGCAGATATCGC
GATAATACGTATATACATAAGGTGGCGCGCGATCTATCGGTATATCCGTTATGGCGGACGTGCGTGAGCGTGAGTCGC
GGCGCATCGCGCACTTCGCGATCGCGTGAAGTCTCGCGACTGCGCGCATGCGTAGC (SEQ ID NO. 616)

Clone Rv61

.....Rv61SP6.seq.....
GGTGATGACGCACTTGTTCGAATGAGTCATTGACTACTCCCGTGGTTGTCTCGCATGGTGGAGTGCCGCGCAGCCT
TGCCCCGANGTCGCGATCGCGTGCAGGGCTTCGGGGAGCAGACTGACCTGCAGATGGAAGTCGTGCCACATGCCCGCGA
ACGGCGAGCTCGATGCTTGTTCGAAGNGCGCANGCGGTTTCGATCTTGTCCGCGTCAACGCAGATCGGATCTCGCC
GCGGTCTGCATGACGATGGGCGCAGGCCCGCTCATGTCCCGTAGACGGGGAGATACGGGCAGCCGCGGATCGAGACCT
ACGTAGCGCGGCGCCCATCGTGCCATCGACGAAGAATGACGGATCGCGCAGCGCCGTGCGTCTCGATGTACGC
GAGATCGCCACGGCAGATCAGCGATGCGCGGGC (SEQ ID NO. 617)

.....Rv61T7.seq.....
CGGTACGCCGGCAACAACGCCTTGTGACGAGCGCGTCCGAGCGGTCTCGGCCCTCCACCGTCATGCACAGCTCCTTC
TCCAGGTCTACGCCGACGTGCGGGTCCACATTTGGTGAGCTTGGCGAATGCCTCGGCAACCTCGTCGAAATGCGCCTCC
GCGTCCGCATCGAAGGTGCGCATGTCAAAGATCAACTCGACGTAGTAGCTAGTTACCGCATCAGGTCACTGTTTGTCTG
GCCTCGGAGTCCGGCCGAACAATGGCCATTTCCCGGACTCTAGAATCCAGTCATCGTCTCGGTGACGACGCTTGGC
GATCACATAGCTCGACCGGATCGGAGAGAATCTGGTTCTCGT (SEQ ID NO. 618)

Clone Rv62

.....Rv62SP6.seq.....
ATACTCAAGCTTAAGCGCAGCAGTACCGGCGGTGCCTGGGCATCCAGCAAAACGGGGAGCTCAACGAACGATTCTTG
AACGAAGGGTCGTCCACCAACCTCAAACCGAACGGTTGCCAGCCCCGGC (SEQ ID NO. 619)

.....Rv62T7.seq.....
GCAAGTCCGCTCAATGTGGTTGTGATCACANGACTACGTGCGCTCAATCAGCTCAAACGTCAACCCCGTGGCGTGCTGC
GCAGATGAAGGTGCGCGCGCCGACGATGTGGCGGAAGCAACAGGTAATAACTGGTTCGGCATGGGTCAACCCCTCATTG
GGCCGTTGCGGATCGGGTGCACGCCCGGAGTGCCGGTCAACTCAACACCGCCTTACCGATCTTTTCGTGCAAAATG
GCGGTCTGTGCGGGTATACGTCCGCGATCCACGAGGCGGAATCCGCTGAGCCGCACTGA (SEQ ID NO. 620)

Clone Rv63

.....Rv63SP6.seq.....
ATACTCAAGCTTCCGCGCCTCAAGCGGCTGAAGGTGGTTCCGGCGTNCCAACNGTCGGGCAACTCGCCGATGGGCATG
GTGCTCGACNCCGTCCCGGTGATCCCGCGGAGCTGCGCCCGATGGTGCAGCTCGACGGCGGCGGTTCCGCNCGTCC
GACTTGAACGACCTGTACCGCAGGGTGTCAACCGCNACNCCNNGTGAAGGCTGATCGATCTGGGTGCGCCGGAA
ATCATCGTCAACAACNAGAACGGATGCTGCNGGAATCCGTGGACGCGCTGTTCGACAATGGCCGCGCGGCGGCGCC
GTCACCGGGCGGGCAACCGTCCGCTCAAGTCGCTTCCGATCTGCTCA (SEQ ID NO. 621)

.....Rv63T7.seq.....
TGCGCATGGCAGTTGTTGCCGGCTTGTGTCGCTTAGCGCGGATTCCACCACATCCCTTGGGAAGTCGTGGGTGCAAT
GATGTAGCGCTTCTCCATCGAGATAGTGGAGCAACGAATCCGTGCGTACGTTGGGTCTGAGTGCAGTGCAGTCTT
GGCGTTGACACCATCTTTGTATTGCGGCGAAGTCGATCATCCGGTAAGCGCGCTTATCGACGCCGCTCTGTGCCGG
GTGGTAATCCGGCCATGCGCTTGCCTCCACCGCGACGTGCAGCGGGCGCACACCGACTTCTCCGGGTGACGGGTGATC
TCGGCGAATCAGAACCTGGCGCGGACACAGCGTCGTGGCTGTACTTGC (SEQ ID NO. 622)

Clone Rv64

.....Rv64SP6.seq.....
TGGGTGATCAGATACTGGCTAGTTGGTGGGTGGGTGATCGAAGATCGCGGTGGCCGGCAGCGTTACTGCGGTGACG
CTGTTAAGCGGTTACGTACTCCACGGCACTCAANGAATTANATCCCGAATCGGCAAAACCTGGCCAGCGTCGAGTCCG
CAGCGCGTGCAGCCCCCAGCTGCGGCATGCTCACATACCACCTCGATCGTGCAGGAGTTGCTGCTCGGCCGAC
CGACCGGCCAGCCGGCGGCAACCGGAGGACCAAGATTACGACACCACCATCGCTAGCCGATCTGGCGCGCGGTGG
(SEQ ID NO. 623)

:::Rv64T7.seq:::

TCGTAGCGGTTGCGACCANTCCGCGGACAGCTCCGCCACGCGACGGGTCTGGGATCACCGCGGTCAAACCACCGAGCGG
CGAGGATCTCTGGCCGTCGACGTGACCGCGCACGCGCGGTGATGGCCAGTCCCAGACCGCGTTCCACTTGGCGTAC
GCGCTGGATGTGTTGTGCCGCAACGGAATCCACCTCAATTATGACCTCGTTGTGGGCGAGCGCGGTATCGTACGCCC
GACCAGGAATCGTCGATGCTATCTCACGTACCGAAGGCTCTCCAGCACACCGCATCCAGAACGTGCACACNGTCG
ACATGTCTCGGCGGATCCGCCTGCAGAACGAACGCCANGTGCGCTGTGCGACACGGGTCTCGCATCACCGCTCGCACGC
GGAGATCGGCACACGCGCAGCGCATCGATCATAATCTCTCGATGCGGTCTCCACCACCGAACAG

(SEQ ID NO. 624)

Clone Rv65

:::Rv65SP6.seq:::

ATACTCAAGCTTCGCTGAGGTGGTGGGCGACGATCACGTACCGCACCGCTGTCTGGTGGCGCTGGATGCCGGCCGGAT
CAACCACGCGTACCTGTTCTCTGGGCGCGTGGTCTCGGAAAGACGTCTGTCAGCGCGTATCCTGGCNCGGTCTGTTGAA
CTGTGCGCAGGGCCCTACCGCAACCCGTGCGGGGTCTGCGAATCCTGCGTTTCGTTGGCGCCCAACGCCCCCGGCAG
CATCGACGTGGTAGAGCTGGATGCCGCCAGCCACGGCGCGTGGACGACACCCCGAGCTGCGGGACCGCGCGTTCTA
TGCGCCGCTCCACTCACGCTACCGGTATTTATCGTCGACGAGGCGCACATGGT

(SEQ ID NO. 625)

:::Rv65T7.seq:::

GCACCTACGCTGGTACAAGACCTTCACAAAATCTGAAATCCTGACCCGATACTTGAACCTGGTCTCGTTCTGGCAATAA
CTCGTTCTGGCGTGCAGGACGCGGCGCAAACGTACTTGGCATCAACGCGTCCGACCTGAATTGGCAGCAAGCGGCGCT
GCTGGCCGGCATGGTGCAATCGACGAGCAGCTCAACCCGTACACCAACCCCGACGGCGCGTGGCCCGCGGAACGT
GGTCTCTGACACCATGATCGAGAACCTTCCCGGGGAGGCGGAGGCGTTGCGTGCCGCCAAGGCCGATCCGCTGGGGT
ACTGCCGAGCCCAATGAGTTGCCGCGCGGTGCATCGCGCGCGGACCG

(SEQ ID NO. 626)

Clone Rv66

:::Rv66SP6.seq:::

ATACTCAAGCTTGATAAAAAGATCGGTGAGCGCATCGATTGCTCCGCCGGGTTTGCCGCTGCGGCGCGGAGCTGC
CGTGACCGTCTATTTGGGTGATCAGATACTGGGCTAGTTCCGTGCGGGTGGGTGATCGAAGATCGCGGTGGCCGCA
GCGTTACTGCGGTGACGGCTGTTAAGCGGTTACGTACCTCCACGGCACTCAAGGAATTAATCCCGAATCGGCAACG
CCTGGCCAGCGTCGAATCCGGCAGCGCCGTGCGGCCAGCACCGCTGCGGCATGCTCACATACCACCTCCATCGCTG
CGGCGAATTGCTCGTGGCCGACCGACCGGCCAGCGGGCGGCAAACCCGGAAGA

(SEQ ID NO. 627)

:::Rv66T7.seq:::

CCTCATCATATGCCGATAGAGCTCTACATATTACAGAGATCACCATGGCTCGTGCGGTCTGGATCGACTCGGGACCAC
CAACTCCGTCGTCTCGGTTCTGGAANGTGGCGACNGGTCTGTCGCGCAACTCCGGAGGGCTCCAGGACCACCCGTC
AATTGTCGCGTTCGCCCGCAACGGTGAGGTGCTGCTCNGCCAGCCCCGCAAGAACAGGCAGTGACCAACGTCGATCGC
ACCGTGCGCTCGGTCAAGCGACCATGGGCAGCGACTGGTCCATAGAGATTGACGCAAGAAATACACGCCCGGAGATCT
CGCCGATTCTGATGAACGACGACCCGAGGCTACTCGGTGANGACATNACGACGCGTTATCACACCCCGCCTNC
TTCAATGACCCACGTCNGGCACCAAGGACCCGGAATCGCGGCTCACTTGNGCGATNGTCNACAACCAACGCGNCGC
CTGGCTACGGGCTCAACAAGGCANAAGACACAATCCGCTCTCGATTGGTG

(SEQ ID NO. 628)

Clone Rv67

:::Rv67SP6.seq:::

ATACTCAAGCTTATCGAGGCGGCGCATACCGAAGCGTGGGAAATCCAGACCGAATACCGCGACGTGCTGGACACTTTG
GCCGGCGAGCTGCTGGAAAAGGAGACCCTGCACCGACCCGAGCTGGAAAGCATCTTCGCTGACGTGAAAAGCGGCCG
CGGCTCACCATGTTTCGACAACCTCGGTGGCCGGATCCCGTCGGACAAACCGCCCATCAAGACACCCGGCGAGTCGCG
ATCGAAGCGGGCGAACCTTGGCCCCAGCCGCTCCCGAGCCGGCGTTCAAGGCGGCGATTGCGCATGCTACCCAAGCC
GCTGAGGCCGCGCGGTCCGACCCGGCCAAACCGGGCACGGCGCAACGGTTGCGCCGCGCGGACCAACCGGTCCGGTGA
CCGAGTACGGTCCCCCAGCCTGACTACCGTGCCCGGGCGGCT

(SEQ ID NO. 629)

:::Rv67T7.seq:::

TGGCCGGGCTGGTAGCCCGCGTATGGCAAGGTTCCGCTCAATGTGGTTGTGATGCAGCAGGACTACGTTTCGCTCAAT
CAGCTCAAACGTACCCCCGTGGCGTGTGCGCAGCATGAAGGTCTGGCGCCCGCACGATGTGGCGAAGGCAACAGGT
AAGAACCTGGTGGCATGGGTTCGAGCCCTCATTGGGCGTTGCGGATCGGGTTGCAGCGCGCCGGAGTGCCGGTCGAA
CTCAACACCGCCTTACCAGATCTTTTCGTCGAAAATGGCGTCGTGTCCGGGTATACGTCCGCGATTCCACAGAGGCG
GAATCCGCTGAGCCGAGCTGATCCGGGCTCGCCGCGGCGTATCCTGGCCTGTGGTGGTTTCGAGCATAACGAGCAG
ATGCGAAT

(SEQ ID NO. 630)

Clone Rv68

.....Rv68SP6.seq:.....
GTCCAGTCAAGCATCGGTCTCTCCGACTACGCCAAGANTGGCGACGTGTCACTGCANACAGCGGANATGGTGGCGCC
TATGCGTCGACGCTCACAAACNGCGGTGANCGCGTTCTGGTCGTGCACCATCGAGCCGTGCCAGCCCGGCCGCGTGCC
GTCAGCCGCATCCACTGGATGCCTTCTCGGNGTTTCAATCANGTACANGCGACGTTCCGCCACCATCGTGCCGGGGCAC
GGTTAGCGAGAAACCGCCGACTTCACCGATTGCCTCGGTGATGCCGTGGAACAGATCGGGCCTATTGTGCGACAGCCAG
TGTGATNCGTATTTGCCGCCGTGCTCCTCGTCGCAACGATGCGAACACAGATCCGTGGNGGACGATAGCGGCTGACAA
NGTGGGGGCAACACAATCACATGCCACATTTCTTCATTTACGCCCACAACCCAGACTTCGTCTCGATGNGCCG

(SEQ ID NO. 631)

.....Rv68T7.seq:.....
CACGCGGTCTGGCCCCGATCCGAAGATCCCTTTGCCGGCGTGCGGGCTCTGCTCGGCGGTGTTGTACACTTCTCGAACA
CCTCGGCACCGACACCACCACCGTNGCTTGAACACCGCCAACATCGGCAGCAGATCTTGATGGTCTTGGTGAATCCCA
CGGTGACTTTGGAGTGGAAGGCCCATACTGATCGCCGCCAGCACATGAGCTAGCGGCAGGAAAACAGCAGCCGC
TCACCTTGCGCAGCAGCGTCNGGTGATATGCCTGGCGCCCTTAATCTCGTGAACCAAGTTGGATTGGGTCAACTGCGAG
CCTTGGGTCTCCGGTGGTGCCGANGTGTANATAAGTCCCGGGTCCGTCAACGTANTGCGCAGGCGGCGGTTACTCGG
CGGGTCAACGAGCCCCGCTCGTGAGCNATCAGCCTTTTGACCAGAACGGGATTCATACTCCGCAGGCGGCCCTCCGAAA
TCGGCACATGTCCTTTGATCGTTCGCAACAN (SEQ ID NO. 632)

Clone Rv69

.....Rv69T7D3.seq:.....
GGCCATGTACATCGGTGGTACAGGTAAACCGCGCCGTGTGCGCGGTCTCGGAGATCAGAACGTGGTGCAGTTGAAC
CGCGGGCTTTAGCCAGTCGCGATAATCGGCGGAAGTCGGCGCCTGCCGCCCCAACTAGCGCGACTCGCCACCTAGCA
CACCGATGGCGAAGGCCATGNTCCGGCCACGCCGCCGCGGTGCATCACCAAGTCATCGACTAGGAAGCTAAGCGACA
NCTTGTGCAGGTGTTCCGGCAGTAGCTGCTCGGAAAATCGGCTGGAACCGCATCAATGGTCCGTCGAATCGAACCG
GTTACCCGATCGTCAAAAAATCTCCGTCCT (SEQ ID NO. 633)

Clone Rv6

.....Rv6SP6.seq:.....
GGGTCTACAACCACCGGGTCTGACTTCTGGGCTTCCACCGCTCGCGCCGTGCGGACAAACAGCGCGGTGGAACCGACA
CTCGTTGTGATGTCCAGCTATCACCTCCGGTAGGCACCCAATCGACCCTACCCGGCTATCTCACCCCGATCTCCAG
GCTCCGCCGATCCATGCGCATCCCGGTCCGGATCCC (SEQ ID NO. 634)

.....Rv6T7.seq:.....
CAGGCATGCAAGCTTGTCTGATTCGGTGGCACTGTGAGACATATGCGCCGCTCCTCCTCATCGCTGCGCTCGGCATCG
TCGCCGGCGGTGATGGCGTCACCTACCCAAGCCGAACGCGAAACGAGAACGTGTTCCATTATTAGGGTGTGAGCACC
AATACCAGATTGCTCACCAGGAATCAGCGCAGCACCAGGACGGATGTGAGCCACCACGCCCATCTGGGGTGGTAGCGG
GGAATACGGCTAACGCGGCTCCGGTGCCGGCAGCCAGCGCAGACCCTCGGCGGGGACACGGCTAACAAACGACGAC
CCATAGTTGTTCTTTGCCGATGGCCGTGTTTGCTGACATATCGGGCGCGGCGCCGGCGCCG

(SEQ ID NO. 635)

Clone Rv70

.....Rv70SP6D2.seq:.....
NCTACGCTGCTGAATGTTGTGCGCCGGAGGANCTCAAGACCCACGCGGTTGTACGCGGACNTGGGACATGTTCAACCG
CCGGA (SEQ ID NO. 636)

.....Rv70T7D3.seq:.....
CTAACCAACAAGCCATGGTGGTTGGCGCCGTGAGAGGTGCGCGGTGCGCACAAACGGGAAGATCGCCTTGAGCGTCGC
TCGACCGCCGCTCGAGTTGGGTGATAACGAAGTACTGATGCCGATCATGTGACGCTGTCCTGCGCATCAGCGTGCAG
CGGCGACCCCTCGACGAGCCTCGGTGCCGCCGCGGCCAGGGCACCAGCTGTTTTAGCGCATTGTGCTCCGCCGGTAAT
AAAGGANGTCGGTTCGCTCCGCTGCTGTGGTTGCGGAATAACATCTTCCCTTCCTGCAACAGGATGAGAATGGTTTAA
ATTGCTC (SEQ ID NO. 637)

Clone Rv71

.....Rv71SP6.seq:.....
CTAAGCTTTCCGGTCCGCCGCCACTAGTACCGGTTGCCGGCCCCGCCGACCTAGAATGTTCCGCCCATTGCCGTTTC
CTCCCGCCGCCGGGTT (SEQ ID NO. 638)

.....Rv71T7.seq:.....
TCTGGTGCCGGGTGTGCCGACGGGTCCGTCCGCCTTGCTTCAGTGATTCTGTGATGCGACCGGCAACGTCCTCGTTG
TTCGGTGTCTATGTGGTCCGTCTCTCCTTGTTCGCATACGATT (SEQ ID NO. 639)

Clone Rv72

.....Rv72SP6D2.seq:.....
GCGATCGNTNACCACAAGGGCGCAACCGTTGCGCGCTCGACTGAACGTGCTGCGGCCTGGAGAACTGGCGCTGCTGCC
ACCTGGTCGGCGCATCGGCACCTTCGAGGACTGGATTTGACGCGTGGCCCGACCTGANGTNGGCGGTGGACNNGTGTG
CACCCGGTTGATTCTCGGCCTTGCCGGGATGCCACCTGCGCCTGGTGGTCGAT (SEQ ID NO. 640)

.....Rv72T7D3.seq:.....
CGTGACCGGACGGGGTGCCGCGCAACCGGTCTTGCCCAATTGCCGGGGACTGGGGCTGGAGTATAAAGCGGGCCTGT
TGCCGGAAGATHAAGTCAAAGCGGTGACCGAGCTGAATCAACATGCGCCGCTGGCGATGGTCGGTGACGGTATTAAACG
ACCGCCAGCGATGAAAGCTGCCGCCATCGGGATTGCAATGGGTAGCGGCACAGACTGGCGCTGGAAACCGCCGACGCA
CATTAAACCATAACCACCTGCGCGGCTGGTGCAAATGATTGAAGTGGCACGNCCTACGCGCAATATCCGCCAGAAC
TCACTATTGCGCTGGG (SEQ ID NO. 641)

Clone Rv73

.....Rv73SP6.seq:.....
ATACTCAAGCTTCTTACCCANAGCATGAACCCCGCCGTCCAATGCCGCCACCGTGGTGCTGTCGGCCGGCCGGGTGCG
GGCACAATCGCCGAGTTCGGCGAACAGATCCTCGAAGGTCTTCACGGCCAGCGATTGTTGCACGTGTGAGCCAGCCAA
GTCACGGTGGTTTGACGCCACACGTTCCGCCACCGCCGCGCCGCGCATTAGGGCATCTAATATAGGTTAGGCTACCCCT
ANTTATTCTGTGGTCAAGGAGGCGAGCCGAACGTGACCTTCCCGATGTGGTTCGCGAGTTCCGCGCGGAAGTGCCGTCA
GCATGGCTGTCCACCGGCATGGGCCCGGTCCGCTGCTGGCCGCGGCCAGGGCGTGGCACGCGCTGGCCGCGCAATAC
ACCGAAATTGCAACGGAACCTCGCAAGCGTGCTCGCTGCGGTGCAGGCAACTCGTGGCAGGGGCCAGCGCCGACGGTT
CGTCNTCCCCATCAACCGTTCCGTATTGGCTAACACCTGCACGGTGGCACCGCAACGCCGCCACAAACGCGCCCC
GGTATAC (SEQ ID NO. 642)

.....Rv73T7.seq:.....
GGCCGAACCTAATCGGTTGTTGGCGGCTGCCGAGTTGGGTCACTCGGGGGGTGTGCACTGGCACATGGTGGGCCGGAT
TCAACGCAACAAAGCCGGTTCGCTGGCTCGCTGGGCGCACACCGCTCACTCGGTGGACAGCTCGCGGTTGGTGACCGC
GCTGGATCGGGCGGTTGTTGCGGCGCTGGCCGAACACCGTCGTGGCGAGCGGCTCGGGGTTTACGTCCAGGTACGCCT
CGACGGTGACGGATCCCGGGGCGGCTCGACAGCACGACGCCCGGCGCCGTAGACCGGATTTGCGCGCAGGTGCAGGA
GTCAGAGGGCCTCGAACTGGTCGGGTTGATGGGCATTCCGCCGCTGGATTGGGACCGACGAAGCCTTTGACCGGCTG
CAATCGGAGCACAACCGGGTGCGTGCGATGTTCCGCGACGCGATCGGTCTGTGCGGGCATGTCCAACAACCTTGAAT
CCCGTCAACATGGTCGAC (SEQ ID NO. 643)

Clone Rv74

.....Rv74SP6.seq:.....
GCTTCCCTGATACTCGACCAGCCCCACTCGGGCCAATACGTGAATGTCCTAGCATTTTTACCCGTTACCGGGCTAG
TCGAGTAGTAGACGATTGATTAGCCTGAACGTACCTCCGACGGCCAGCTGACGAACGGGTTTGACGGA
(SEQ ID NO. 644)

.....Rv74T7D3.seq:.....
TCAGCTGTCTGTAGAAGGGCTGGCGATACTGTGCACTGTCTGATATCGCNCGTNGTGGGACTATNCAGNCCATNANG
ATGCGGTTTCNGNNNTGCAGAGNATCCTGGNACACATNCGGTTCAGGTTAATCANCATCGCGANTTNTNCGTNTTCG
ATTANTCTGCTAACGNNCTNNNAGTGCCTGCGGGTCGACTCTAGAG (SEQ ID NO. 645)

Clone Rv75

.....Rv75SP6D2.seq:.....
NCTCTGCCGGGNCAGAGCGCAGAGTCGGACGGTTCGTGATCGTGAAGCGACCNTGCGATGANAGATATCGNTNAC
ACTGCTCANAAACTTCGGATCATCGNTGATACACAGGCCAACGGGTAGCGGTTGTCCAACGGCTTCGTCAACGANATG
GGATCGTGACGANCTACGCTCGCAGGATATGTCGCGNACCGNCTAGANAN (SEQ ID NO. 646)

.....Rv75T7D3.seq:.....
CACTTCATGCTCGTGCGTTGGCNTCGATTTGCNCGAGNGGTTAGCTCCTCGAGTGNGTGACGTATCACTCCGGCNGAC
TANCCGTATCNGCGTCCCGCACCGGTCACTGGTCTAGCCACACGGGGAGAAATNCNCGACCGGNGCTATCGACCNAT
CACGGCTGTGCGNNAAGATAGNACGCC (SEQ ID NO. 647)

Clone Rv76

.....Rv76SP6.seq:.....
ATACTCAAGCTTGCCAACCGCCACCCTGCATCCGGGGGGCGAGCACTGCTCCGCCGACCAGTACGAACCAACCTGCGG
TGCCCAGGCCATTGACAAATGTGCTGGTCGGCGCCCGCAGTTCTAGCACAGCAACGCCGCGCCACCACAGGGGCG

(SEQ ID NO. 648)

.....Rv76T7.seq:.....
CGGTGCGGTGTGCTTGGCGGGCTCGGTATCAACACCGCCACGAAATGGGGCACAAGAAGGATTTCGTGGAGCGGTGGC
TGTCCAAGATCACCTCGCCAGACCTGCTACGGGCACTTCTACATCGAGCACAACCGTGGCCATCAGTCCGGGTGT
CCACACCGGAAGACCCGGCGTCGGCGCGGTTTCGGCAAACTTTGTGGGATTTCCCGCCCCCCC (SEQ ID NO. 649)

Clone Rv77

.....Rv77SP6.seq:.....
AATACTCAAGCTTCGCGGAGGTGGTGGGGCAGGAGCACGTACCCGCGCCGCTGTGCGGTGGCGCTGGATGCCGGCCGGA
TCAACCACGCGTACCTGTTCTCTGGGCGCGTGGCTGCGGAAAGACGTGTCAGCGCGTATCCTGGCGCGGTGCTTGA
ACTGTGCGCAGGGCCCTACCGCAACCCGTGCGGGGTCTGCGAATCCTGCGTTTCGTTGGCGCCCAACGCCCCCGGCA
GCATCGACGTGGTAGAGCTGGATGCCGCCAGCCACGGCGCGTGGAGCAACCCCGCGAGCTGCGGGACCGCC

(SEQ ID NO. 650)

.....Rv77T7.seq:.....
GATGGCACTCACGCTGGACAAGACCTTCACAAATCTGAAATCCTGACCCGATACTTGAACCTGGTCTCGTTTCGGCAA
TAACTCGTTTCGGCGTGCAGGACCGCGCGCAACGTACTTCGGCATCAACGCGTCCGACCTGAAATTGGCAGCAAACCG
GCGCTGCTGGGCGGGCATGGTGCAATCCGAACAAGCACGCTCAACCCGTACACCAACCCGAAGGGCCGCTGGCCCG
CGGGAACCTTGTCTCCA (SEQ ID NO. 651)

Clone Rv78

.....Rv78SP6.seq:.....
AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTCTGGGCGTCTGGTGCC
GGCTGCCGGTGCAGGAAGTGGATTTTACTGCCATCTCTCGCGACCTGAGGTGGTCCAGGCTTACAACACCGACCCA
CTCGTGCACCACGGACGGGTTCGGCCGGGATTGGCCGCGCGTCTGCANGTGGGCGAGACCATGCCGCGCGGANCA
CCGGCATTGACCGCGCCGCTGCTAGTCTGCACGGCACCGATGACCGGCTGATCCCCATCGAAGGCAGCCGTGCGCTG
GTCNAATGTNTNGGATCNGCCGACGTGCANCTGAANGANTATCCCCGGCTGTNCCACNAGGTGTTCAACGAACCGGAN
CGCAACCAAGTG (SEQ ID NO. 652)

.....Rv78T7.seq:.....
CAAGGCATACGCCAAGACCCAAGGGATCGCAGTCACCTCCGTCAACGGCCTGGTCCGCCGGCCACGGGTCCGTGCAGGA
GACGTGGCTGGCCATGCAAAGCGCCGCGCCTTATCAGGAACGCCCCGGCTTGTGCGCTTTTCTGCATCGACACATT
TCCGGAGGTGTTGTGGTTGGCGCANCGCGCAGACAGGCCTGGGATGGCGTGCATCGTTCATCGGGAATGCGATGGC
AACACTGAACTACGAGCGCATCTGCGCCAGCATGACTGTTTCGACTACGTCGTGCTTGGCGACGGGGANGTAGCGTT
CACCAAGCTGGCCTTGGCCCTGGCGAATGACCTGCGGTTGACGACTCCCGGGACTAACCCGCGGTANTGAGCAAGGAC
AGATTCTGCGCACACCCTCTCGCTGGTCGACCTTGACA (SEQ ID NO. 653)

Clone Rv79

.....Rv79SP6.seq:.....
AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGCCGGTGATCTGGGTGGC
CAACTCGGCGGGCACCATCTCCATCAGCANGCAAACGCTCGGGCTTCGGCGACAGCGATCGCGTCTGCGATNGTTTG
TTCGGCGGCGTCTCCGCGGCCCTGCACCCGGAAGCCGCCCAAGGTGTTGACNCTTTGCGGGGTGAAGCCGATGTGTGC
CATCACCGGGATNCCCGCGCGGTGAGACANGCGATTGCTCGGCCACCCGCTCACCGCCCTCGANCTTGACNGCATG
TGCGCCGCCGTCTTGAAGAAACCGGTGGCGGNGGCAACCC (SEQ ID NO. 654)

.....Rv79T7.seq:.....
CGTTGAGATCCAGCTGCGCACTGTGCAGCGCCTCGGTGGTCTGCTCGGCCTGCCGGGATAACTCGTTGAGCTTGCCCA
GCGCGTCTGTCGGCCGGATCAGCCAGCACATTGCGCGCCAGGACGCCGGAGGAGACGGTGAAGCTCGAAAGAAACCTA
TGGCGGACCGCATGATTACACGCGCGATCAACCACCTCTGGTCGAGCCTCAAAATTTGCTTCTTAAACGGGCCATCG
ACGGATGACGTCGAGCTGGTTAGGTCTCAAACAGGTTACGAAACGATCTCGGAATTGTCCAAAAGGGGAAGTTAAGA
AAATGGATAGATTTCTACCATTTCTGCTGTGGACGATCGTACTTCTGCTATAGGGCTCCAGGGGCATCGACACGCAACG
ACCTTACGCGACACCGGATCCGCGCTGGCGGCGGAACGGCACANGCGCAACCGAAGGGCCAATCCGACATCGG

(SEQ ID NO. 655)

.....Rv263T7.seq:.....
CGTAATCACGATCCCGCTGAGACACTTGACCTTACGGCCGAAGTGACTTCGCTGCTGCTATGCCGACACCCGATTTC
ATACGCTGCTGTACACGACGGCCGGCCGGTGGCTCCATCACGCTCAACCGCCCGAACAGCTCAACACCATCGTCC
CGCCCATGCCGACGAGATCGAGGCCGCTATCGGGTTGGTCGAACGCGACCAGGACATCAAGGTCATCNTNCTGCGCG
GTGGCGGGCGCGCTTCTCCGGCGG (SEQ ID NO. 297)

Clone Rv264

.....Rv264SP6.seq:.....
CAAGCTTAAGCTGGTTCGGGCCACTCCATGAGCCGTAGTGCAATGGTTCGTGCACGGCGAGGCCGAACCTTGCCATAAA
CATCCCTGACGAAAGTCTCCGGCAAGCCGATTGCTTCTTCGGGCCGCTTCTTGTGGATTGTCCGATAACCCGGTCCCT
CATGCTGGAAGTTGTGCGCACTCTTTCCTTCCGCGATGTGGGCTAACGACTCGTCATTGAGCAAGAAGTACGTGCACA
GGCATCGTCCGCCGGGCTTCAGCACGCGGGAGATCTCGTCCAGATAGTGCTCCAGTCCGGNGGGAACATGTGGGTG
AACACCGAGGTNAGAAACACNCATCCAACGACGCATCCGGGATATGAAAGCGAAA (SEQ ID NO. 298)

.....Rv264T7.seq:.....
TATGGTCTTCGTGACGACGACGTCGTAGGCGCCATGAGCCAGCGACTGAAGCCGCGCCATGCCTGCACGGCCCGCTC
ATCCAGCGAGGCGGCCATCTCCCGCAGATAGCCTGCCGCTCGGCGCGCACGCTGTCCGGATCGCGTCCGAGCTCGTC
GGCCAGCGCACGCGCGCTCGTCATACCATCGGGCATCCAGCAGTTGGGTAACCTCAACGGGGTTCGGTCGCTAGCGG
CGTCATTGATTAGCAACAATACCGATGCGCTGCAGCAACTTTCGAGTCCGATGCGGCCCACCTCCCGTGCAGTCAC
TGGCTAGCCCCCGTCATGCCGTTGTGTGATGGCACGGCAGCGGGTCTGTAACCTGCGGTCTCAGTCGCTGG
(SEQ ID NO. 299)

Clone Rv265

.....Rv265SP6.seq:.....
GCTTAGCGGTCTTGCTCGAACCAGACATTGCGTGCCACTCATGAGCGGGTGGCGGTGCGGGTCTTACACATCT
(SEQ ID NO. 300)
.....Rv265T7.seq:.....
GTATCTGGCGCTCTCGAATATCCTTGACGTCGCGGGTCCACCCAGATAGATCGCAGCGCCCTGCAATGGAGTTC
CCTTTATGGCCTCTCTAGCCTCCCGCTTGATCGGCTCGACCCGAGAGATGCCCTCGGGCGTTGCGGGATCTCCCTCCA
(SEQ ID NO. 301)

Clone Rv266

.....Rv266SP6.seq:.....
CTTCACGCCGATCCGCGACCGCGAACGCGACGGTGACGGTGGGCGACAAGGTTTCGGTTGGTCGCCGCGCGCTGGGCG
ATATCAGCTACCCGGTTTCGAGGTGTTTCGGCGACCGGACGGTGCTGCAGACATTCTTGAGCGTCTCGACCGGCCCG
ATTTCGGCTTCAACATCGTGACGCCGTATTTTCGGCGGTACCGCTCGGCGCCGAGTCGAAGGCGGCCCTGAGCTAAAGCC
GGGCAATTGGCGGAGTGGTAAACAAGTTCGGTGACTTCGGTTGACCGACTCGACGGGTCGATCTGGGCGCGCTGGACC
GGTATCTGCGTTTCGTTGGGGATCGGGCCNACCGCNANTTGCGTTGCGANCTGATTCCGGTGGAGCTCCAATCTGACTT
CCGG (SEQ ID NO. 302)

.....Rv266T7.seq:.....
GCAGCTACCGACCTAGCGACGAGTGTGTTTCGACGCTCGAATGTGAACGTTTCGGCGTGATTTCGGCGCGCGGGTCCC
GCTCTCAGCGCACGTTTCGGCGCGGAGNGGCTAGTCCCTGGTTAAGCAATGTCTCGGTGCGCGCCAGCAGCGCGCATG
TCGCCAACCCTCNACCGGTTGCGCATGTCCGGTACCGACGGAACGACGGCGCGATCCGGATGTTCTTGTGTCGTCG
GATCCTTTTCGATACGGGAACGACCCCCGCTCGGTACCGCGGATACCAACGTCCTTAGCCAANGCTACNGTCCGGCG
CGCGGTCCCGGGAACACGTCGAAGCTGATGAANTAACCACCTTGGGCTCGGTCCAAGANGCGATCTTGGACTCCTT
AACCGCTGATNCAA (SEQ ID NO. 303)

Clone Rv267

.....Rv267IS1081N60.seq:.....
TCCCCATCGGCGCGGACCGTTTGAAAGTCCAAGCACGGGTGGGATGGAATCGACGACAGTTGAGCGCGCTCGGTGGC
CGTGGTCAGCAGCTGTTTCGGAACGCACCGAGTACATCCCTTCGACATCTCACCGACGTGGCACGGGCGACATCAAC
AGGAAGATTGACGAATCCCTCGCAGGCGCGGCACGTCCGACGGCCAACGCCAACTACGGGGCCACCGGATCCTCCG
CTCACGCACCGCCAAAGCCAGGCTCANCCACCCAAGTCGGCCCCGCGCTCTCCCTCGCCCCCTGGTCTCCGGGGCCTT
GTTAAACAACCTACCGGAAGTCCACCAATCCTCGCTGCATCTCGACACCGTCCGCTCACTCCCTTCTCCCGCCCCCTC
TCCACACNACACCTCTTGATTAAGTACGCGAGCGGTCACTTTTCGTGCGAGCAAATTCGCAATCCGGCCGCTCG
CCGCCAGAGAT (SEQ ID NO. 304)

.....Rv267SP6.seq:.....

CGGAAAGTGGATACTCCCAGCAGGTAGCAGGTCGCCACCACGCTGGTCAGTGCGCGTTTACGCTCGCTTGC GGCGCTGC
AGCAGCCAGTCCGGGAAATAGCTGCCCTGGCGCAGCTTGGGGATCGCGACGTGATGGTTGCGGCACGGGTGTCGCAA
ATCACGGTGGCGGTAGCCGTTGCGCTGATTGGACCGCTCATCGCTGCGTTGCGGCTAGCCCGCCCCGCACAGGGCGTC
GGCTTCAGCCCCCATCAAGGCGGCGA (SEQ ID NO. 305)

.....Rv267T7.seq:.....
GGCCGAGTCCAGCACTTCGCACTATGTGCAGACCAAANACCCGGTGGTCGCCGCGCTGCGGCAGCGGCTGGCAACGGC
GCCGGTGATCACCGAGTGGTGCGNAGTTGCCGACCGGCAGTTTCGCCGCGGGCTTACTACGAGAAGGGCCTGCGCGACG
TCATCAGGTATCACGTGTCGATGACGTCGAGCGTTAACTTCCCCGACCAGACGGCGACCTCGCCGATGGACCCCGCGT
TGTAACCTGGTGTGGGCGCAAGCTAACGCCCGCGCANGCTATCGGTACTCGGTGCGAAGCGCAGCCGGGGTTCGCAAGCGC
TAGCGGGCAAGGTCGCGACGATCTCGGTACCTGGACCAACTACGGCGCTGCTGCCGCCACCGAATAGTNGTGCCCG
GCTACCGGCTGGTGGATTCCACGGGACATGTGGTTCGGACCTGCCGGCAGCGGTGGAAGTGAAGANGCTGGTCT
(SEQ ID NO. 306)

Clone Rv268
.....Rv268SP6.seq:.....
AGCTTCAAGGACATCGTCATCGCAGACAAAACCGCGAGCTAGGTGCGCATCCGGGAAGCATCGCGACACCGTGGCGCC
GAGCGCCGCTGCCGGCAGGCCGATTAGGCGGGCAGATTAGCCCGCCGCGGCTCCGGCTCCGATTACGGCGCCCGAA
TGGCGTCACCGGCTGGTAACCACGCTTGC CGCGCTTGGCGGGCGGCTGCCGGATCAGGTGGTATATGCCGACAAAGCC
TGCCTGATCGGTATCACCAACGGTGACAGCAGCGGTTGTGCACCATCGCNAACGCCACCCCGGTCTCCGGGTCTGT
CAN (SEQ ID NO. 307)

.....Rv268T7.seq:.....
GCTCGCGGTCCAGCAGCAGACGTGTCTGACCCCGACGCCCCGGCCGCGGTACCGAAACCGGATCGGCCCGCCGATGGC
CGCGGCCACGGCGTCTGCCCTTACCCGGCCCGGATACAGCAGCCACACCTCGCGGGAACGCTGAATCGCCGGCAGGGT
CAAGGTGATTCGGCGTGGCGCGGTTTCGCGAATCGTCCACCGCCACCACCATGCGGGTGTCTCGAAGACGCGGGGC
TGTGCGGGAACAGCGAGTTAATGTGGCCCTCGGGCCCCATGCCAGCAGGTGGACGTGGAATTGCGGCCCGGTCACC
TGGTGCGGCACTGGCGGCC (SEQ ID NO. 308)

Clone Rv269
.....Rv269SP6.seq:.....
AGCTTGTGATCGTCCGGCAGCGTCCGGCGAGTCAAGTCAAGCCAGTCCGGTCTCCTCTCCGACTACGGCCAAGAAC
TGGGCGACGGTGTGATGCATACAGCGGANACTGGTGGCGCCCTAGGCGAGCGACCGCTCACAAACGGCGGTGACC
GCGTTCTGGTCTGTCACCATCGAGCCGTGCCATCCCGGCCGCGTGGCGTCAGCCGCATCCACTGGATGCCCTTCTCG
GCGTTTCAATCAGGTACAGGCGACGTTGCCANCATCGTGCCGGGGCANGG (SEQ ID NO. 309)

.....Rv269T7.seq:.....
TTGGTGATCATCGNCCCAACGACCCCGAGGCGATGTTCTTGACACCCGAGGAGTGTGCGAAGCTGGGGCTGGCCTTCG
CCGCCGATCCGTCTCAGCAGCTGGCGAAGCTGTGCGGGTGAGGAAATTGCGAGGCTCGTCAACGGTGTCTTACTTG
TTACCAACGACTACTAATGGGATCTGCTGCTGTCCAAGACCGGCTGGTCAGANGCCGATGTGATGGCGCAGATCGAC
CTGCGGGTGACCACATTGGGTCTAAGGGTGTGATTTGGTAGAACCTGACGCACCACCATCCAGTGGCGGTTGGTC
CCCGAAACAGCCAGACCGA (SEQ ID NO. 310)

Clone Rv270
.....Rv26SP6.seq:.....
GGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACGCCAAGCT
ATTTAGGTGACACTATAGAATACTCAAGCTTGATTTTGATCATCATGATGATCATCACCCGAAGTGTGGTAGCCGCGAG
TGGTTATCGTGGGTACCGTCTGCTTTCCATGGGCGCCTTTTCGGGCTTTCCGTATTGGTCTGGCAGGACATTCTGG
GTATCGAGTTGTACTGGATGGTGTGGCGATGTGCGGTGATCTGCTCCTGGCGGTGGGATCCGACTACAATCTGCTGC
TGATTTCCCGGTTGAAAGAGGAAATTGGGGCCGATTGAACACCGGAATTATCCGTGCCATGGCTGGTACCGGGGGAG
TGGTGACGGCTGCCGGCATGGTGTTCGCCGTTACCATGTGCTTGTGTTGAGCGATTGCGGAATT
(SEQ ID NO. 311)

.....Rv26T7.seq:.....
CAGGCATGCAAGCTTGGCGTGCCGTTCCAACCCGAATTGGCTTTTCGGCGCCATCGGTGAGGACGGCGTGCGGGTGCTC
AACGACGAGCTCGTCCGCGGGACACACCTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTA
CAACGCCGCGCGGAACGCTTCCGCCGCGGGCGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTGCATGAC
GGCATCGCCACCGGAGCGACGGCCAAGGCGGCGTGCCAGGTGTCNCCGGGGCGCAG (SEQ ID NO. 312)

Clone Rv270

.....Rv270SP6.seq:.....
GGCATCTTGGCCGCCATGTTAGCCACACTGCCACCGGTATAGAAGCGATGCGCACCGTCCTGCCAGCACATTGCGGC
GTCCTCCCTGGAAAGCAAGATAACCAAGCTCATGCCGTGGTTGTGGGTGGCGTGGTTTGGTTTGGGTAACCTTGG
(SEQ ID NO. 313)

.....Rv270T7.seq:.....
TCGGCTAATAATCGTCGACGCCGGCCTCCTCTGCAATCGCCTTGGCGGTGCGCGGGTGTCAACGGTGATCATCACGG
TGCGGATGCTCATTTCGGCGCATTTTCGTGCAATCGTTCCCGTATGCCACCTTGACGATGTCCTTCAGATGGACGACGC
CGATGGCCCGCGCGCTGCTGTTATCGGTCCATTCCGCAACGACTAGGGGTGTCCCCCGCGGAGCTGATGCCGTGCGAC
AATGGCACCCACCTCCTCGGTGGGGTGGGCACCGTGATCGCGAACCCTTTCATCACCGCAGCCGCGGCACCTTGCGG
ATTCGACGGATG (SEQ ID NO. 314)

Clone Rv271

.....Rv271SP6.seq:.....
CTCAAGCTTGGAGGCGTGGCGATCGCGGTCCAAGGCGCGCTCTCCGAGCACAACGAGCGAAGACNGCTCGGCGACGGA
GCCTTTATCGACNTCCGTTCCGGGCTGGCTGACGGCGGCNAAATAATGCTGGACTCGTTGTTGTGCGACGGTGCCGTGGC
GAGCCGAGCGCCGTGAGATGTACGACCGGGTGGTCTATGTGCCGCGGTTGGTGAGTTTCCACGACCTGACCATCGAAG
ATCCGCCGCATCCGCTGCTGGCGCGGATGCGCCGGTGGCTCAACTAATTCTACGGCGGGCGAACTGGGTNATCCCTTCN
CCACCGTCGG (SEQ ID NO. 315)

.....Rv271T7.seq:.....
CCTAGGTCAACCGTACCGTCATCGGATCGGGGTGACCGCACAGATGGACTGGAGCTTCGGCGAGGTTCATCGCCTATG
CCTCGCGGGGGGTGACGCTGACCCCGGGTGACGTGTTCCGGCTCGGGCACGGTGCCACCTGCACGCTCGTCGAAGCAC
CTCAGGCCACCGGAAATCATTCCCGGGTGGCTGCAACGACTGCGACGTGGTCACCTCCAGGTGCAAGGGCTGGGCGA
GACGATGACAGCCGTCCGGACGAGCGGCACTCCTTTCCGTTGGCTCTTCGGCCGAATCCGGACGCCGAACCCGACCG
GCGCGGGGTCAACCCGGCACCGACGCGGGTGCCGTTTACCCGCGGGTGCACAAATCCCGACGGGTATGGGCTTTGAC
CTGCCGACGGGGGA (SEQ ID NO. 316)

Clone Rv272

.....Rv272SP6.seq:.....
AGCTTGGCGTGACACCAACACAGGGCACTTAAGATGGCAATGCGCCGCTACCTGCACGTTTTCGCGATGTCAGAGGA
TGCCGAGGGGAGAAATGCGAGCACGGCCGCTGACGTTGCTCACCGCTTTGGCGGGGTGACATTGGTGGTGGTTGC
GGGCTGCGAGGCCCCGAGTCTAGGCCGAAGCATATAGCGCGGCCGACCGCATTTTCGTCTGACCGCAAGCGCGACCTCA
GCCGACGCGGTGGAGCTACTGCTGCGCGCCATCACGCCGCTAGGGCTCCGGCGGCGTGCAGCAACGTGGGTTTGG
CGAAGTGCCTACCCGGGTCCGGCAGGCAACCGAT (SEQ ID NO. 317)

.....Rv272T7.seq:.....
TCATGCCGTGGACCGACCATCGGAGTTAGTTGCCGAACCGCGGGACCACCGCAAGCACCCGGTCTGGTTCGCGCACC
GCGTCGGCCAACCGCTTGAGCACCAACACGCCGCGAGCCCTCGCCGCGCACGAATCCATCCGCGTTGGCGTCGAAGCTG
TTGCATCGGCCGGTGGGTGACAGCGCCGACCACTTGGACAGCGCGATGGCGGTGAACGGTGACAAGGTGAGCTGCACC
CCGCCCGCAATGCCACGTGGTTTACGCGAGGCGAAGCTCTGACACGCCAAGTGAATTGCCACCAGCGACGACGAAC
AAGCGGTATCTACGGCGATGG (SEQ ID NO. 318)

Clone Rv273

.....Rv273SP6.seq:.....
GGGTGACTTTCTGCAAGGCGAGGCTACACCGTCGTCGTCGTTGATGCGATAGCCATCCCGTCGGGCTACTCGCCAT
CACCGATCAGCTTCGCCCCGAAGCCGCGTGGTGATTTCCGCTGCGACCAAATGAACGGGGCCAAACCGGTATTGCT
TACCGGCGACAACCGGGCCACCGCCGATCGGCTCGGTGTTGAGTTGGCAT (SEQ ID NO. 319)

.....Rv273T7.seq:.....
AATCCGAATCCTGACCGATACTTGAACCTGGTCTCGTTCCGCAATAACTCGTCGGCGTGACAGGACGGCGGCAACG
TACTTCGGCATCAACGCGTCCGACCTGAATTGGCAGCAAGCGGCGCTGCTGGCCGGCATGGTGCAATCTAACAGCACG
CTCTTCCCGTACACCAACCCGACGGCGCGTGGCCCGGGCGGAACGTGGTCTCGACACCATGATCGAAAAACCTTC
CCGGGGAGGCGGATGC (SEQ ID NO. 320)

Clone Rv274

.....Rv274SP6.seq:.....
TTCCGAATTTGGGTCCNGGTCATATGACCCTCATGGAAGAAGAAGCGGCCGCCCGCGCCCGTGGGACGGCGAATGA
AAACCCTCACCCAGGCCGATTGAACGCCGACAAGACGGTGGAGCAGGTGGAAGACGTCTGGACGGTCTGGGTAAGA

CCATGGCCGAGCTGAACAGCTCGCTGTCACAGCTGAACAGCACCGTGGAGCGCTTGGAGGACGGTCTGGACCATCTCG
AAGGTACCCTGCACAGCCTGGACGATCTCGCGAAACGGCTCATCGTGTGGTCGAGCCGGTGGAAGCCATCGTCGATC
GGATCGACTACATCGTGAGCCTCGGCGAAACGGTGATGTACCGCTGTCCGGTC (SEQ ID NO. 321)

::::::::::Rv274T7.seq::::::::::

NCTCGATCTTGGGGTACGTTTCGATGAGGCTGCTGACCAACAACCCGGCCAAAGCGGGTGGGACTGGATGGATACGGATT
GCACATCATCGAGCGCGTGCCGCTGCCGGTGCGGGCCAAACGCGGAAGAACATCCGTTACCTGATGACCAAGCGTGACA
AATTGGGGCAGCACTTGGCTGGGTGGACGATTTTACGAATCCGTGCATCTGCCCGGAGAATTCGGCGGTGCCCTTGT
GAAGGTGGCGCCGGGTGCCGGATCTGCCGTGCTGGATCGTCTGGTGTGCGGCTGGCGATTGTGCCAGCAGCTGGC
ACGGAAGATCTGCGACGCGCTGTTGGACGGCGCCGCAAGTGGCCGCCGGGTGTGGCCTCGATGACCGACTGTGGTT
CGGGTGCTCCGCGCATCGATAT (SEQ ID NO. 322)

Clone Rv275

::::::::::Rv275SP6.seq::::::::::

TCATCCCGACCAAAACGCGAGCTAGGTCGGCATCCGGGAAGCATCGCGACACCGTGGCGCCGAGCGCGCTGCCGGCAG
GCCGATTAGGCGGGCATATTATCCCGCCGCGGCTCCCGGCTCCGAGTACGGCGCCCCGAATGGCGTCAACGGCTGGTA
ACCGCTCTTGCGCGCCTGGGCGGCGGCCTGCCGGATCAGGTGGTAGATGCCNACAAAGCCTGCGTGATCGGTCATCAC
CAACGGTGACAGCAGCCGGTTGTGCACCAAGCGCGAACGCCACCCCGGTCTCCGGGTCTGTCCAACCGATCGACCGCC
CAAGCCACATGAACAAACCCCGGCATCACGTTGCCGATCGGCATACCGTGA (SEQ ID NO. 323)

::::::::::Rv275T7.seq::::::::::

TTGGCGGGTTGGCCAGCAGCCCGCGGTGACGGCGACGATGCTGGGTGGTTGCGGCCCTGCGCCACCGCGGCTTGC
ATGCTGGTTGGCTGTCTTGGGACGATCCCGAAATAGTCCACGCGGATCTGGTGATTTTGGGGCTACCCGCGATTACC
CCGCGCGGCTCGACGAGTTTTTGGCCTGGACTACCCGCGTGGCCAATCTGCTGAACTCGCGGCCGGTGGTGGCCTGGA
ATGTCGAGCGCCGTTACCTACGTGACCTGATGGATCGGGGGGTGCCGACCGTGCCCGGCGATGTGTATGTGCCGGGAN
AGCCGGTCCGGTTGCCACGCAAAGGCCATGTCTTCGTGCGTCCGACCATCGGTACCGGGACACGGCGCTGTATTGCC
GGTTCGCTGCCGAGTTCGTGCGCAACTGCACGNGCGGGCCAGCGGTGCTCGTTCCNCCGGAGGTTCCGGTGACG
ATGATCGTGTGGTCTCCCT (SEQ ID NO. 324)

Clone Rv276

::::::::::Rv276SP6.seq::::::::::

GTAGGAGAGAACAAGACCGTCGATAGGACACGTGTTACGCCGGTAGCTGTCATTGGTATGGGGTGCCGCTGCCGGGG
GGCATCTACTACCCGATCGGTTGTGGGAGGCGTTGCTGCGGGGCGACAATCTGGTCACCGAGATCCCGCCGACCGC
TGGGACATCTACGAGTACTACGACCCCGAACCCGGCGTGCCCGGACGCACCGACTGCAAATGGGGCGCGTACCTCGAT
AACGTCGGCGACTTTGATCCCGAGTTCTTCGGGATCGGGGAGAAAGAAACGATAGCGATCGATCCGCAGCACCGCTTG
TTGCTGGAAACCTCTGGGAAGCCATGGAACACGGCGGGCTAACACCGAACCATATGCCTCCCGACANGGGTTTTCTG
GGGGTT (SEQ ID NO. 325)

::::::::::Rv276T7.seq::::::::::

CGAACTGAGCCCATAGAAAGGCAGCGACTAATTCGCTGGGCAAATAGGAAGACCCTTTGTCCTGCCACGTATATTTGT
CGACCTCGTTGCGAAGGAAGCGGCTGCGATTGGTGCCCTTTTCCCTGGAGAATCTCTGCCCGGAGCAGGAAGTCTTAT
GAGTTGACAAGCAGGGGCGCGCCTTCGCCGAAATCACATTCTTGGTCTCGTGAAATGAGAGCGCTCCCAGGTGCGC
GATGCTGCCGAGCGCCCGCCACGATACGACGCCATCGCGCCTTGGGCGCGCTCTTCGACCACCGCCAGGTTGTGGTG
CGTGGCGATCTTCATGATCGCGTCCATCTCGCAGGCCACCCGGCATAGTGAACGGGGACCATGGCCTCGGTTGCGGG
TGAA (SEQ ID NO. 326)

Clone Rv277

::::::::::Rv277SP6.seq::::::::::

CTTAGACGCCACCTCCGGGCGGAGCTCCACGGGGTGGATAAGTACGGCCGGATGTGGCCGCAATGGGAAGTTGTTGCC
CGCTTGACTGTCCGGGTTAACGCCGATTCCACCACATCCCTTGCGAAAGGCCGTTGGGTT (SEQ ID NO. 327)

::::::::::Rv277T7.seq::::::::::

GATCGCGATCGTCGATGTGGCCATCCGGCTTGGCGTCGACCCGCGTAAGGCAGACCAGATGGTTCGCGGCACGGTCAA
CCTGCCACACGCACTGGTAAGACTGCCCGCGTCGCGGTATTCGCGGTTGGTGAAAAGGCCGATGCTGCCGTTGCCGCG
GGGCTGATGCTGTCCGATCGAGATCTGATCGAGAGGATCAGGGCGGCTGGCTGGAATTCGATGCCCGCATCGCGAT
ACCGGATT (SEQ ID NO. 328)

Clone Rv278

.....Rv278SP6.seq.....
AGCTTACGCCGCTTTCGCTTCNGATTGGGACGCCGCATCGAAAGCGCAGTTGGAAGCGCGGCGCCCGGCTGGTTCGAG
CTGCTCAAGCAGCCGCAATCCCAGCCCATGCCCCTTGAGGAGCAAGTGGTTTCGATCTTCTGGGCACCGCGGTCAC
CTGGACTCGGTGCCCGTCAAGGATGTCGGCGGTTTCAAACCGAATTACTGGACCACATGCGGGC (SEQ ID NO. 329)

.....Rv278T7.seq.....
CGACGGGACCTCGTCGCATCTCCATAGCCCGCCACACCTTCAGTTGCTCACCAGGAATCCAACCGGTATAAGGTCGGC
GAAGCGCTCGGCATTGGTCATCGGGATATGCCGCTCGGGACGGTCAGATGCCCTCGGGTCGNGCCAGCACTCCTCAGG
CTTCGTCGGGGTGGTCGCGACCGCATGGGCCACATCGCATTACCCAGGTCTGCGCGAATCACCAGCAGGTANACGGTT
CCTTTCCTAAGCAACACCGAAATTCAGGACCCGAATGCTCCGGGAAACATGTCACGGTAAGTCCGGTATTCCGGGT
ACCGGTTGAGCATTGA (SEQ ID NO. 330)

Clone Rv279

.....Rv279SP6.seq.....
CGGCATCGGTTTGGGCTGTCACCAGCAGTTGGTAGTTCTTCACTACTGTTGTTTCGAGCGTCGAGCCGCGCGCTGTC
GAGGTGCGCCGACGCGTACCCGCCAGGCGGTCAGGGTGCCCTTCCAGTCCACGCGNGCTGTGGTCGGCTAACCGCTTA
TCTTCAATCGAGACNATCGCCAGCTTCATCGTGTGGCGATCTTGTCCGAGGGCACCTCGAACCGGCGCTGCGANTAC
AGCCACGCGATCGTGTGCCCTTCGCGTCGACCATCGTCGATACCGCAGGCACTTGCCCTCGAGCAGTGGGCCGAT
CCGTTGGCAACGACCTCAGAGGCAGGATTGGACATCAGCCCTAGCCCGCCTGCG (SEQ ID NO. 331)

.....Rv279T7.seq.....
CCGTCGANGCCGCGGACTTGGCTTGACCGACCAACATGGCCTGAGGGTGTTCAACAAGACCGTGCCCGACGGGCTG
AACATCACCATTGAGCGGCATGAGCCACGCCACCGAGTTCATCATGTTGATCGCCGAAAACCATTTGGCGGGTAGCGGAA
GAACGGTCGAGGTGCTCTACACCGAGTATTCGAAGTCGAAAGGCCAACCGCTGCTCAACGGCGTCAACATCATTTTCG
ACGGGTTTCTGCGAGGGAGGATGCCACGATGAATGGATCCAGGTGCTGTTGATCGCGTCGATCATCGGTTGCTGTT
CTACCTGTTGCGGTGCGGCCGAAGCGCGCGGTCCGTGCCTGGGTCAAGGTGGGCTATGTCTTGTTCGTGCTCCCGGCA
TCTATGCCGTGCTGAGA (SEQ ID NO. 332)

Clone Rv27

.....Rv27SP6.seq.....
TTACACGNCTGCTTCCGGCTCGTATGTTGTGTGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGAC
CATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTTTGGAGCGTCGCGCGGGGCGAGCTTCGCCGG
CAATTTACTAGCGAGAAGTCTGGCCCCGATNCGGATCTGACCGAAGTCGCTGCGGTGCAGCCACCCCTCATTGGCGAT
GGCGCCGACNATGGCGCCTGGACCGATCTTGTCCGCTTGCCGACGGNGACGCGGTANGTGGTCAAGTCCGGTCTACN
CTTGGGCGCTTTCGCGACGGTCCCAGCGTGGTCGCGGTTGCGCCGCGGAAAGCGGCGGGTCCGGTGCCATCAGGAATG
CCTCACCGCCGCGGCACTGNACGGCCAGTGCCGCGGCGATGTGNGCCATCGGGACATCATGCTCGCGTTCTACTCTCT
CGACC (SEQ ID NO. 333)

.....Rv27T7.seq.....
CAGGCATGCAAGCTTTGTACACCAAGTGTTCGACAGGCGCTCCATCCGGCGAGTGGATACTCCAGCAGGTAGCA
GGTCGCCACCACGCTGGTCAGTGCGGTTCAAGTTCGCTTGGCGCGCTGCAGCAGCCAGTCCGGGAAATAGCTGCCCTG
GCGCAGCTTGGGGATCGCGACGTCGATGGTTGCGGCACGGGTGTCGAAATCAGGTGGCGGTAGCCGTTGCGCTGATT
GGACCGCTCATCGTGCCTGCGGTAGCCCGCCCCGCACAGGGCGTCGGCTTCAGCCCCCATCAAGGCGG
(SEQ ID NO. 334)

Clone Rv280

.....Rv280SP6.seq.....
AGCTTAGCCAGTTTTTCTACTCTTGGGCCCCACCCACAGTGCTTCGACGGTACGGTCACCCATGATGGCCATCCAGT
TGGCATCGGTGAGCTGATAAATGCCAGCTGGTTTCGCCAACCCGGTAGCGATCTTGGCGCGCTGCTTGTGTCAGTGA
TACCTATCGAGCAAGACAGCCCGGTTTGCAGCAAGATGACTTTTCGGATCTCTTCGGCGACTTCGATGGGGTCGTGCG
GAGTCCCGGGCGCCACCGCGAGGTAAGCCTCGTCCCAGCCCCATACCTCGACCGGGTATCCCAGGTGCGCGAATAACG
CCACCACCTCTCGGACGCCGCGTGTAGGCGGCTGGGTTTCGACGGCAAGAAGTGGCCTCAGGGCATCGTCGCGCGCGG
TCCCAACGGCNTGCCGGCGCGCACACCGTAGGCGCGGGGCTC (SEQ ID NO. 335)

.....Rv280T7.seq.....
CCGGCGGAAGTACAGCGTGCTGGTGGTGGCGCATGGCACCGCGGGCAGCAAAGCGCACTTCTCCGGGGACGACAGCAA
GCGACCGCTAGACAAGAGGGGTGCTGCGCAGGCAGAAGCGTTGGTACCACAGCTGCTGGCGTTCCGGCGCCACCGATGT
TTATGCCCGCGACCGGTTGCGCTGCCACCAGACGATGGAGCCACTCGCCGCGGAAGTGAACGTGACCATACACAACGA
GCCCACCTGACCGAAGAGTCTACGCCAACACCCCAACGCGGCGGACACCGAGTGCTGCAGATCGTCGAGCAAGT

AGGCACACCCGTGATCTGCACGCAGGGCAAGGTCATTCCCGATCTGATCACGTGGTGGTGCGAGCGCGACCGTGTGCC
CCCCACAGTCCCGCAATCGCAAAGGCAGCACGTTGGTGT (SEQ ID NO. 336)

Clone Rv281

:::Rv281SP6.seq:::

GTATGGTCAGCTGTCCATCCGGCGCTGTCGGCCGAGCTGCCAGATCTCGTCAGCCGTAACCGGGTTGCGGGATCCACG
CGTGCGGGTTGTCTAC (SEQ ID NO. 337)

:::Rv281T7.seq:::

CCGACTTTCGCGGGTACCCGCTCAACTTTGTGTCNACCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAACT
ACTTCATCTGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGACCCAGTACT
ACATCATTCGCACGGAGAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACC
TGGTTCAACAACTTGAAGGTGATTGTTAACCTGGGCTACGCGACCCGGCCTATGGTTATTCGACCTCGCCGCCAA
TGTTGCGACTCCGTTGCGTTGTTCCAGAANGTCAGCCG (SEQ ID NO. 338)

Clone Rv282

:::Rv282SP6.seq:::

GCACCGATGTCGGCGAGCACTTCGTCAACTTCCAGGGGTGCCCGCACCAAGTATTCGACGAGTATTCGGTCGGGCC
GCCGCCCGGGTGC CGCGCAGGTGGTCATCCTGGCGCGGGGGCTGGGACTCGCGCGCTACCGGCTGCCTCGGC
(SEQ ID NO. 339)

:::Rv282T7.seq:::

TGCACCAACTTACTGAGCATGCTAACGCTGGTCGTGCGGGTCTTGTTCGCGCTGTCGGCAGGGCACACGCTCGGGG
CGTAGCTGGGAGAGGCCCGGTCAAGCCCGAGAGCAGTGCTCAGTCCGCCAGCTTGACCGACTTTCGATGAGAACGC
GCTTCTCGCGTATTGAAGTGGCGTGCTGACGGTCGCTGAGCAGCGCTCGCCGAGTGGCGCGCTGATTCTTTCATCG
AGCCAGGACGCGCATTCGTGTTCCGCCG (SEQ ID NO. 340)

Clone Rv283

:::Rv283SP6.seq:::

AGCTTACGGCCGGTCGACGCGACGAGTGGTTCATGACACCACAAACCGTCAACGCCTACTACAACCCGGGGATGAACG
AAATCGTCTTCCCGCAGCGATTTTACAGCCACCATTTTCGATCCGCAGGCCGACGAGGCCGCCAACTACGGCGGGAT
CGGGGCGCGTGATCGGGCACGATGATCGGGCACGGTTTCGACGATAGGGCGCCAAATACGANGGCGACGCAATCTGGT
CNATTGGTGGATCGA (SEQ ID NO. 341)

:::Rv283T7.seq:::

ATGTCGTCACGTCAACCAATCGCGAGGACCAATCATGCCGCCAGGGCGGCCAACCCAATGGTGGCCGCGAAGCGG
CAGCTCGATCGCAGCGCGGAGGTGCCGGCCGCCAGTTGATTACGAACAGGGTGAGGTCTAGGCCGGCAGGATAGTG
ACGAACGCAAGACCTATATCTGCCGTGGAGTAAGAAATCGAGTAGCCGGTCGACCAACGGAAGCGAAAGTGTCGCGA
TGTTGATGAGCGTCGCCGGTTGTGGCGCGGTGGC (SEQ ID NO. 342)

Clone Rv284

:::Rv284SP6.seq:::

AGCTTACACAGCGTGCCGATGCTGTTTCGCNACACCTCCCTACTATGCGCAATTGCGCGACACGGGTGGCATCAACAG
GGCGATAAGGTGGACATCGCTGGGGTGAACGTCGGGCTGGTGCGCTCGCTGGCAATCCGCGGCAACCGCGTGTGATC
GGATTCTCGTTGCCCGGCAAGACAATCGGGATGCAAAGCCGGGCAGCAATTGCGACCGACACCATTTGGCCGTAAG
AACCTGGAAATCGAACCCCGCGGTTCCGAGCCGTTGAAACCCAACGGTTTCTGCGGTTGGCGCAGAACTACGCCA
TACCAAATCTATGACGCGTTCGTC (SEQ ID NO. 343)

:::Rv284T7.seq:::

CTGCCGCGGTGGCGGTGACGCGCTGGCAAGTACCGCACCGCGCTCCGTTTCATCGGCAGGCTCCCCGAAAAGGGCC
CTGGCAACAGAAGGTGATCAATGAGCTCCCGCAGACCTTCGCCGATCTGGGACCGACATACGTGAAGTTCGGCCAGAT
CATCGCTCCAGCCCGGAGCATTCGGTGAGTCGCTGTCGCGGGGAATTCCGCGGCTGCTCGACCGGGTGGCCCGG
CAAAACCGACGAGGTGCACAAGCTCTTCGTCGAGGAACCTCGGCGACGAGCCGGCCCGCTGTTGCCTCTTCGAGG
AAGAACCCTTCGCTGTCGCTCCATCGCCCAAGTGCATACGCGACCTGCGCAGCGGCGAAGAAGTGTGGTCAAGATC
CACGGCCGGCATCCGCCCGCGGTTT (SEQ ID NO. 344)

Clone Rv285

:::Rv285SP6.seq:::

GATCGTGCCGGCCCCCGGCGGCAGTAGCAGATCAGCTCGTGAATCGCGGCAACCAGTCCAGTTCGATTCCATACG
GGCGCCGTCAATCAACTCTGCGAACATCGCGATCGGCACCGGAAACCGGCGAGCCGCGTCAGCCAGCGCAACCAGCAC
CGGGATCGGATGAATCATCAATATTATCAAGTGATTTCTGATGGCATCGAGCTCGGTGATCTTGGTCTCGGGGGCCA
GCTCGCCGTGCGGCAGCTCGTTCGATCCGGCGGCCGAGCGCATAGACCGCAAATAGTCCGCTCGCTTTTCGCGCGGCA
AGAGTCGGATGCCGTAATATANGTTTCTGGCGGCCGTGCGCGTGATCNACTCGGTGATTGATACGCCTGTTTCATCTC
GGTCATGCCGTCTC (SEQ ID NO. 345)

::::::::::Rv285T7.seq::::::::::
GGTGGCGCAATGACCGAAACACCCAGCCCCGAAACCCCGGCGGCCCGGCGGCCCGGCGCACAATCGTTCTGTG
GAGCGGCCCATCCAGACCGTTGGGCGCCGTAAGGAGGCCGTGGTACGAGTGGGCTGGTCCCGGCACCGGCAAGTTC
GACCTCAACGGCCGAGCTTGGAGGACTACTTCCCAAACAAGGTGCACACAGCAGTTGATCAAGGCACCCCTGGTCACC
GTGGATCGGGTGGAAAGTTTCGACATCTTGGCCACCTGGGCGGCGGCGGCCGTGGGTTCATGGCCGGCGCGCTGCG
CCTGGGTATCGCCCGGGCATTGATTCTNGTATCGCCGGATGACCGGCCGCGCTGAATAANGCCGGCTTCTTGACCGT
GATCCACGCGCCACCGAACGCAA (SEQ ID NO. 346)

Clone Rv286

::::::::::Rv286SP6.seq::::::::::
CACATAGATTACTCAAGCTTCGAACCAGCGGCCCTATCACGTATCCCCGCTGAGACCTTGACCTTAGGGCCGAAGT
GACTTCGCTGCTGCTATGCCGACACCCGATTTCCAGACGCTGCTGTACACGACGGCCGGCCGGTGGCCACCATCAC
GCTCAACCGCCCGGAACAGCTCAACACCATCGTCCCGCCATGCCCGACGAGATCGAGGCCGTATCGGGTTGGCCGA
GCGCGACCAAGGACATCAAGGTTCGTGCTGCGCGGTGCCGGCCGCGCTTCTCCGGCGGTACAACCTTCGGCGCGG
GTTCCAACATTGGGGCAT (SEQ ID NO. 347)

::::::::::Rv286T7.seq::::::::::
TCAGGACGCTTATGGTTGGCAGATGGTCGCCCTGGCGTGAATACGCGGAGCGCATGAGCTCACCGGTTCCGAACAA
CGTATCGAAGAAGCTCGCACTGCTGGCAGATGGTATCTCCGATGTGGTTGTAATTTGTATCCCAACTCTAACTGTGCT
ATCGGATCAGCGTGAATATCGAGATATTGCGAATGCGATGACAGGCCGCCATTGGTTTATTTCGCTTACGCTTCCCGG
GTTTCGATTCTGCTGATGCACTGCCGAAACGCGGATATGATTGTTGAAACCGTATCTAACGCAATTATTGATGTGGT
AGGCGGCAGCTGCCGTTTTGTGCTGTGGGCTATTTCATCGGGTGGGGGTGTTTGGCTATGCCCTCTGCTCCCAT
(SEQ ID NO. 348)

Clone Rv287

::::::::::Rv287SP6.seq::::::::::
CGCAGCTGTGCGCGATCTGGTCCGGAATACCTAGCTCCAGGTTCTGAGTGAGATGAGTGCGGCCATCGAAGTGTGT
CAATGTACTCCAGGATGTCAGGTGCCAGGCCGTGGCGAGGATCTTGGGCACCGCCGCCATGACTTGGTTCGAAGTCGG
CGAACGGGGCGAGCACGCTGGCGTCTGTGTC (SEQ ID NO. 349)

::::::::::Rv287T7.seq::::::::::
GTAGTTCGTTTCATCCAAACAGTGCGGTACCGCTCAAGCGGATCACCGACTTCACCGGGCGCGATCCACCCAGCC
ACCGGATGCTTATGCTCTCGGGTGGCGGCCACCGTGGGTCAACTCAACTATCCGACGCCGCACTGAAGCATCGACAG
CAATGCCGTGTATAGATTCCCTCGCGGTTCAGAGGGGTCCAGCAGGGGCCCGGAAAGATACCAGGGGCGCCGTC
GGACCGA (SEQ ID NO. 350)

Clone Rv288

::::::::::Rv288SP6.seq::::::::::
TCCGCTCGCTTCTCCGAGAGGTTGAGTGCCAACGCTCTGCCGATGCCCGAAGCCGGCCCCGGTGATGACGGCGACCTT
GCCTTCGAATGAGCTCATTTGACTACTCCCCGTGGTTGTCCCTGCGATTGGTGGAGGTGGCCGCGCAGCCTTGCCCCG
AGGTGGGCGATCGCGTCTCGGGCTTCGGGGAGCAGACTGACCTGCAGATGGAAGTCGTGCCACATGCCCGCGAACCGG
CGATGCTCGATGCTTGTTCGAAGCGGCGCAGGCGGTTTCGATCTTGTCCGCTCAACACNGATCGGATCGTCGCC
CGGGTCTGCATGACGAATGGGCG (SEQ ID NO. 351)

::::::::::Rv288T7.seq::::::::::
ATGGGAGGCCACCGATTACCATCTTGACACACCGATTCCGGGCTATTGATGTCCACGTTCCGGTCCGCGAACCGCGCT
GTGGCTGCTGCTGGCCAAAGGCGGAGGCGATACCGAAGTCAGTGCCCAAGCTTGGGTTCCACGCTCGCGCAGCCACGC
CGTCACCTTTCCACGAGACCTCACCTGCCGATCCGAAATGGAATCGGCCGTGACGGAATTGGCGCAGCGAACACTCAA
CGAGGTGGTGGCTTCGTCGCGAACCGTCACCCGAGTCGCGGTACCGTGCGCAGCGCGACGTTCTACACCCGCAACAA
GATCCGAAAGCTGCAAGCTCCAGCACCGATCCGACGTCATCACCGTGCCGCCCGGACGTTCTTGAACCTATTGC
AGCTGGAATCGGCCGTCCGGTTGCTGGGAATTGCNGTTAAGAACTGGGCCT (SEQ ID NO. 352)

Clone Rv289

:::Rv289SP6.seq:::

GCTTTGCGCGCTTCTCCGAGAGGTTGGAGTGCCAACGCTCTGCCGATGCCCCGAGCCGGCCCCGGTGATGACGGCGACC
TTGCCTTCGAATGAGCTCATTGACTACTCCCCGTGGTTGTCCCTGCCGATTGGTGGAGGTGGCCGCGCAGCCTTGCCC
CGAGGTCGCGGATCGCGTGCGGGCTTCGGGGAGCAAACCTGACCTGCAGATGGAAGTCGTGCCACATGCCCGCGAACC
GGCGATGCTCGATGCTTGTTCGAAGCGGCGCAGCGGTTTCGATCTGTCCGCGTCAACGCAGATCGGATCGTCGCC
CGCGGGTCTGCATGAAGAAT (SEQ ID NO. 353)

:::Rv289T7.seq:::

CTCACGCAGCCACGCCGTACCTTTCCACGAAGACCTCACCTGCCGATCCGAAATGGAATCGGCCGTGACGGAAATTG
GCGCAGCGAAACACTCAACGAGGTGGTGGCTTCGTGCGGAACCGTCACCCGAGTCGCGGTACCGTGCGCACGGCGAC
GTTCTACACCCGCACCAACATCCGAAAGCTGCAAGCTCCAGCACCGATCCCGACGTCATCACCGCTGCCGCCCGGCA
CGTTCTTGACCTATTCGAGCTGGATCGGCCGTCCGGTTGCTGGGAGTGCGGTTAGAACTGGCCTAGAAACCGGCGG
GCACACCGCACCTGGGCGGGN (SEQ ID NO. 354)

Clone Rv28

:::Rv28SP6.seq:::

TGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACG
CCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGATGCCGCCGAAACCGAGCGTGAGCACGCCGCCAGCCACC
ACNCGCGGGTCGGGCGCCGGGCCCCGGGTCGCCANGCTGCTCCGCTCGGTGATGGCACGCCACCGCGACACACCGGC
TGCGCTACGTGAGCCATACCGGGCGGAGCTACATCGGCTCGGCCGCCAGTGTTGCGGCCCTCTTTCGAAGTCGAAG
TCGATACCGATTGCGCATCCGCGGCCGCA (SEQ ID NO. 355)

:::Rv28T7.seq:::

CAGGCATGCAAGCTTCACGTCCGTACGGCTCGGGTACGCTTCGGTCGCAGTGTGCGAGTGATAGATGACGACCGGGAC
CTCGTCTGCATCTTCCATAGCCCGCCACACCTTCAGTTGCTCACCGGAATCCAACCGGTAGAAGGTGGCGAGCGCTC
GGCATTGGTCATCGGGATATGCCGCTCGGGACGGTCAGAACCCTCGGGTCGGGCCAGCACTCCGAGGCTTCGTCGGG
GTGGTCGCGACGCGCATGGGCCACC (SEQ ID NO. 356)

Clone Rv290

:::Rv290SP6.seq:::

GCTTGTCTATCGTCCCGGCCAGGTCCGGCCAGTCAAGGTGGAAGGCCAGTCCGGTCTCCTCTCCGACTACGGCCAAGA
ACTGGGCGACGGTGTGAGTGCAGACGAGCGGAACTGGTGGCGCCCTAGGCGAGCGACCGCCTCACAACCGGCGGTGA
CCGCGTTCTGGTGTGACCATCGAGCCGTGCCAGCCCGGCGGTGCGGTGAGCCGCATCCACTGGATGCCCTTCT
CGGCGGTTTCAATCAGGTACAGGCGACGTTGCCACCATCGTGCCGGGACAGGTTAGCGAGAAACCGCCGACTTCAC
GATTGCCTCGGTGATGCCGTGAAACAGATCGGCCT (SEQ ID NO. 357)

:::Rv290T7.seq:::

GCGCGCCATGTTGAGGTTGTCCGACGGTGACGACGGTGAACCACAACCTGTTTGACCTGTCCGCACACACCGTGTGGAT
CGGCGAGCGGACCCGACAAATCGATGGCGCGCACATCGCGTTTGCCAGGTGATTGCTAATCCGGTCGGGGTCAAGTT
GGGCCCCAATGACCCCGAACTGGCGTGGAGTACGTGAGCGGCTCGACCCGCAACAATAAGCCGGCGGCTGAC
TTGGTGAGCAGGATGGGCAACCACAAGGTCCGCGATCTGTTGCCACCGATCGTGGAGAACGTCCATGCCACCGGGCAT
CAGGTCACTTGGC (SEQ ID NO. 358)

Clone Rv291

:::Rv291SP6.seq:::

TTGCCTTCCATGCCGAGCAAGGTGACTCAGCGATGACGAATTGTTCTTCTTCGCGGGTGTGCTGCTGGTTGCGGGC
TATGAGAGCACTGCTCATATGATTAGCACATTGTTTCTGACGCTGGCCGACTATCCAGATCAGCTGACACTCCTTGCG
CAGCAACCAGACCTGATCCCGCCGGCGATCGAGGA (SEQ ID NO. 359)

:::Rv291T7.seq:::

CGACGCTGGGCCAACTGCGACCACAGGTCCTGGTATGGCAGGACATGGCCGGGTTACGCGGCGCCAATACCG
(SEQ ID NO. 360)

Clone Rv292

:::Rv292SP6.seq:::

TAACGACTCGGGTCCAGCGACCGCCAAACACNAACGGCCGACNACGTGGGCCAGGGTCGCGGCCCTCCCTACAAAC
AGGATCGGTTGCCTGCGAACGACAGGCTCCGGTGGCGGCTTGGGCGCCGTGCTCGTCCAGCGTCCGGTCCCGGGTCCG

CCGGCGACGCTTGTTCCTCCATACTCGCCCCCTAATCTCGAGGCAGCCCGTACCCGCAGGCAACCTCCCAAAAATGC
AATCCCCCAAAATGCAATGCGTCNAGCTATTTCTCACACCGACCGCTAGTTGCGGATCANAAATCCGTTGGGCGCGGA
(SEQ ID NO. 361)

::::::::::Rv292T7.seq::::::::::
CNTGGCGGTGGGTGCGGTGTCGAACACGACCACACTTCTTTGCGGTTGCGTGATCTCGACACCGGCCGCGAGCCGACC
ACCATGCGCGCGTAGATCGGCGATCAGCGCGTCGGCTATCGCCTGGGTGCCGCCACCAGGAATCGGCCAGCCGACCGA
ATGGGCCAGCGTTGCCATCATCAGTCCGGCGCCGGCCGACACCAAGTGACGGCAACGGTGAAATCNCGTGGGCGGCAAC
GCCGGTGAACAACGCGCGGGCATCCTCGCCGCCAGCGACCGCCAGGCAGGGGTGCCCTGGGCCAGCATCCGACGCC
GAGACNCAGGACCGANCCAGTG (SEQ ID NO. 362)

Clone Rv293

::::::::::Rv293SP6.seq::::::::::
GCTTTTCNGATCGCAGCGAGTCGTACCCGCGCCGGTCACCTTCGTGGATATCGCCGGCCTGGTCAAGGGGGCGTCCGA
GGGAGCCGGGCTGGGTAACAAGTTCTTGCTCATATCCGGAATGCNACGCCATTTGTGAGGTGGTGCGGGTGTTCGT
CAACAACNACTTGACTCATGTACCGGACGGGTCGATCCCCANTCCGACATTGAGGTGCTCGANACCGAGCTGATCCT
GGCANATCTGCAACCCTGGAGCGGGCCACGGGCCGGTGGAGAAGGAANCGCCGACCAACAAGGCGCGCAAGCCGGT
CTACGACGCGGCACTGCGTGCCAGCAGGTGCTCGACGCCGGCAANACGCTGTTGCCGCGGGGGTGGATGCCG
(SEQ ID NO. 363)

::::::::::Rv293T7.seq::::::::::
GTCGTACGCCATTNGTCGGTGTGCGCATACCACTACGACGCGCCGGGCACCTGACGCGGCGGCCGCGACCACTCGGTG
GCCATCGCCATCGTCTGCCACCCGGTCAACGGACGCACCTTCTCTGGCCGACGTAGTGCGCCACCCGCGCCCGTTG
CGTCCCATCNATCCGGTCAACATGAGCAGCGCCAACACCGAGCGGTACATGACATCGCTGTGGAACCACTGACAGATT
CCGCGGCCCATGATGATCATCGACCGTCTCCGGATTGCGTTCGCGTTGCGGGCGAAATTCCTTGGCAAACCGGATTGC
CTGCGCGGCCGCGCACACCGGTGATCGACTCCTGCCAGGCCGGGGTGTCTGCTGGGTTCGGTTCGTGGTACCGGT
(SEQ ID NO. 364)

Clone Rv294

::::::::::Rv294SP6.seq::::::::::
GCGAGGCGGTATCGCTTCCCGTGTACCGGCGACCGCCAGCCGAGAAGCTCGTTTTCCAGTGTTGCTGGGGATTCTC
ACGCTGCTGCTGANTGCGTGCCANACCGCTTCCGCTTCGGGTTACAACGAGCCGCGGGGCTACGATCGTGCGACGCTG
AANTTGGTGTTCTCCATGGACTTGGGGATGTGCCCTGAACCGGTTACCTACNACTCCAAGCTGGCGCCGTCTCGTCCG
CAGGTGCTTGCCTTGCATAGCCGGGAGGCCCGGATCCGCAATGACGGATTCCATGCCAACGCTCCGAGTTGCATGCGG
ATCGAATACNAATTGATCACCA (SEQ ID NO. 365)

::::::::::Rv294T7.seq::::::::::
TGGGTCTTGCCGGCGAGCCAGCGAAGTCGCTAGCGTGCGCGTGTCTTCTGGCTTCGGATCTATCCTCGTTACATGAC
CGGCACCGTGTGGACGTGACTGGCGGCCGGTTCATATGACACCGAGATCATTGCCACGGTACGGAATTCGTCAAGA
AGGAAATCTTTCCNATGCACCGGCCCTCGAACGTGGCAACAGCTACCCGCAAGAAATCGTCGATCGGCTGGGTGTTA
TTGGCTTGCTCGGTGCGCGGCTGCAAGGGTATCGACACCACCGAGTTCATTCTCGGGCGTGCCGGCGCATTCGAGCTG
GCGGTGCGCGCTGCCAGCACCGTCATAAGTACTTGANGATGGTCAAACGTGCGACGAACCGCCACCAGTCGCTGCC
GAACGG (SEQ ID NO. 366)

Clone Rv295

::::::::::Rv295SP6.seq::::::::::
TAGATGCCCAAGCTTGCCNTTANAGACCTCGTCGACCAAGCACGGACGCGACCGTCGAAGGTGGCGAATCCGGGCTTG
GCGTCNACCCGCGTAAGGCAGACCAGATGGTTGCGGGCACGGTCAACCTGCCACACGGCACTGGTAAGACTGCCCGCG
TCGCGGTATTGCGGGTTGGTGAAAAGGCCGATGCTGCCGTTGCCGCGGGGGCGGATGTTGTGCGGAGTGACGATCTGA
TCGAGAGGATTGAGGGCGGCTGGCTGGA (SEQ ID NO. 367)

::::::::::Rv295T7.seq::::::::::
TCTCCACGGCGTGATCAAGGTACCGCCGGGATGTTGCGCAATGGCAGGTTGTTGCCCGGCTTGATGTCTGCGTTAG
CGCCGGATTCCACCACATCCCCTTGCAGAAAGTCCGTTGGGTGCAATGATGTAGCGCTTCTCCCCATCGAGATAGTGG
AGCAACGCAATCCGTGCGGTACGGTTCGGGTCGTAATGATGTGCGCGACCTTGGCGTTGACACCATCTTTGTCATTG
CGGCGAAAGTCGATCATCCGGTAAGCGCGCTTATGACCGCCGCTTTGTGCCGGTNGGTAATCCGGCC
(SEQ ID NO. 368)

Clone Rv296

.....Rv296SP6.seq.....
GCCCCGTTTCGATCGGGCATGTCCGCAGTCGTCTTACCGGAGGCGGTCTGTGGCCGCGCTAATCGGCGTCGGCGCCGAC
AAGATGTGGGATATCCGCAATCGGGGCGTCATCCCTGCCGGCGCGCTCCCCCGCTCCGAGCCTTCGTGACGCAATC
GAGGCAAGTCACGACGCGGATGAGGGGCAGCAGTGAATTACAGCGAGGTCGAGCTGTTGAGTCGCGCTCATCAACTGT
TCGCCGGAACAGTCGGCGACCGGGGTTGGATGCGGGCACCACACCCTACGGGGGATCTGCTGTCTCGGGCTGCCGAC
CTGAATGTNGGTGCGGGCANCGCCGTATCNACTCCCGTGAACACAGCCGGGGC (SEQ ID NO. 369)

.....Rv296T7.seq.....
CTCGGCGTGGATATCGGTGTAGCCGGCGCCGGTGAANGTCGGCTCCTTACGTCCACTCGACAACAGCTCATAGCGATC
CAACCAGTANGCAACCGCCTTCAGCAGTACAACCGCGCCGGCGAACACTGCGAGTTGAACGCGAGCTGCCTGGGTCAG
CATGCCCTCTGCCGTTGTGACCCGAAGGCCGCCGAACAGGTAATGCGTCAACAGGCTCGCTAGAAACGCCAGAACCAC
GGCCACGAACAGCCAGTTCAGCACCGACCGGTAGAACGGCAGATCGAAGACGAAAAACCCAATGTCATAGCCGAATT
CGGGGTCCACGATGCCAAAGGTGCCCCGTGTACAACACTGAACCTTCACCCA (SEQ ID NO. 370)

Clone Rv29

.....Rv29SP6.seq.....
TCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACGCCAA
GCTATTTAGGTGACACTATAGAATACTCAAGCTTCAGTCCGTACGGCTCGGGTACGCTTCGGTTCGAGTGTGCGAGT
GATAGATGACGACCGGGACCTCGTCGGCATCTTCCATAGCCCCGCCACACCTTCAGTTGCTCACCAGGAATCCAACCGGT
AGAAGGTGCGCGAGCGCTCGGCATTGGTCATCGGGATATGCCGCTCGGGACGGTCAGAGCCCTCGGGTCCGGCCAGCA
CTCCGACGGCTTCGTGCGGGTGGTTCGCGACGCGCATGGGCCACCATCGCATTACCCAGGTCTGCGCGAATCACCAGCA
CGTAGACGGTTCTTTCTAAGCAACACCGAAGTTTCAGGACCGAATGCTCCGGGAAACATGTCA (SEQ ID NO. 371)

.....Rv29T7.seq.....
CAGGCATGCAAGCTTGATGCCGCCGAAACCGAGCGTGAGCACGCCGCCAGCCACCACGCCCGGGTTCGGGCGCCGGGCC
CGGGCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCGCGACACCACCGGCTGCGCTACGTGAGCCATACCGG
GCGGAGCTCCATCCGCTCGGCCGCCAGTGTCCGGGCCCTC (SEQ ID NO. 372)

Clone Rv2

.....Rv2SP6.seq.....
CCTGCATCCGGCTCGTATGTTGTGTGGAATTGTGANCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTA
CGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTCCAATCCCCCTGCCCTGATACGCGTCGGCAACCGTGAA
CGCGATCTCGGCGACCGTTCGGATCGGTTTCATCCCGCACAAAACGCGCGTCGGCTACGGGGTTCGCTTCGGTTCGTCAT
CACCCAGACGAAGTGGTCGACGTAGTCGACTTCCGACAGGTAGTGCATCAACGCCGGACTGGGAACACNAGCCGACAT
GAACCGTCGATACAGCGTCTCNCGGAGAAGTGGATGTGTCCGTGCACGGTCCGCTCGCGGTACCGGGCAGCACGGG
GCGTAACATCAGTTGAGTCCGCTCGGCAAGCCGTACCGGAATCGGGGAGACGA (SEQ ID NO. 373)

.....Rv2T7.seq.....
CAAGATGATCGCCGGTGCCACCCGATCCGTGCTCGGTTCAGCGCGAACGTGCTTTCGGGTCCGGCGACCACCATGTC
GCACGCACCGACCGAGGCCGAACCCGCCGGCCGCACATGCCCGTTGATGGCGCCGACCAACCGGCAGCGGCGACTCGAC
GATGGCGCGCAACAGCGCCGTCAATTCGCCGCCCGCGCCACCGCCATCCGGTACGGATCACCACCACCGCCGGC
CTCGCTGAGGTCCGCGCCGGCGCAGAACGTTCCGCCGGTATGCCCGAGCACGACCGCCGACCGCGGATCTGCTTC
GGCCGCACTCAGCCCTTGATGTAGTTGGGTGACGAGCGTGTGACAGCGCGTTGCGGTTGTGCGGAGAGTTAGTGT
CAGCCTGGCGAAGGGGCCGCCGAGGCGGGGCCAGCGTAGTCGACGGGGCTG (SEQ ID NO. 374)

Clone Rv301

.....Rv301SP6.seq.....
CTCAAGCTTCGATCGACAGTACTCCCGCCTTGGGTCTGGTCTTCGAGCTGGTTCGGTCATGGTTCGGACCTGCTGGTAGT
GGGGATCTAACGCAACATGGTTCGGGATTCATCATGGTGTACCCGTGATACCCATTTCGAGCTGCCGGTGAACCCCCGC
GATGCCGGGATTTCCAGCCGCACTAGGATGTCTAGCCGGCCAGCCGTGCCGCCGGAATTCGGGATGTTCCGGTATACC
ACCGATCGGCAATCTGCNTATCCGCCGATGCTCGAAGCGTAGCCACCCCAAACCAACCACTGTGACNACAATC

.....Rv301T7.seq.....
TGAATTTCCCGATCCACAATCTCGGTTTCAGATACAGGTGCGCCATACCCCTTACTTCGGCAACGCTGGGCGGATTGGC
CCTGCCGCTGCAGCAGACCATCGACGCCATCGAATTGCCGGCAATCTCGTTTCAGCCAATCCATACCCATCGACATTCC
GCCGATCGACATCCCGGCCCTCCACTATCAACGGAATTTGATGTGCGGAGGTCTGCGCGATCGATGTGTCCGTGACAT
TCCGG (SEQ ID NO. 376)

Clone Rv302

.....Rv302SP6.seq:.....
TACTCAAGCTTGAACGCTGCGAGCGAGCCCATGTAGAGCGTTTGGTACCAAACCGATCGGTGGGCCAACTTGCCATGG
GCTCACAGCGGCTATCGCGAGCGGTAGCCGATCATCGGCCAGGCGACGGTGGCCTGAGCGGCAGGGGTTGCCCTTATC
CATCCTCTTGCGGCATGGTTGCCGAGGGAGTGCCGGTAAGTCTGGTGGCAACCTGGCCCGCTGCGGGTTGGGTTTCG
GATTCCCTCGGCTAGTAAGGTGCTCGCCTGGTGTACAAACGAATCGCTAGAGAGCTCTTATCGGGAGTGGCCGTCGCG
ATCGTTGCGCTGCCGCTGGCGATCGCGTTCCGCNTTACCGCCACCGGAACGTCCCAAGGTGCGCTCATCGGGCTCTAC
GGCGCCATCTTCGCCGATTCTTCCNGCCGTGTTCCGGTG (SEQ ID NO. 377)

.....Rv302T7.seq:.....
GCGGTGTCTGAACCTTCGCCGTTCCCTCCAGCGCATTGAGCTTCAGCCCGACCGGCAGGTAGGGAGTGGCATGCGGT
CCTTCGCCCGGACCCCGCTGGCTAAATAGCCACCCCGAGCGCGGTACGGTCTTTGCACCGGGACGACGGCATACCG
GCAGCGGAACATCGCCGCGGGCTGCAGCGTGAACGTGCAATACGAGTGAACAGTGTGCGCGCTAAAAACCCGAGC
CGGCGGTGCTTCGGTAATCAACGGCTCCTGCGCAACCAGCTGCAANTCNCCGGTGCCACCGGCGTTGACAATCTTGA
TNTCGGCGACCTCGCGCACCAN (SEQ ID NO. 378)

Clone Rv303

.....Rv303SP6.seq:.....
TACTCAGCTTCGGCTCAGGTGGTGTGCTGGTAAAGTTCNCTGAACGGTGCAGGTTTCGACAATGTGGTGCCGGTTTCG
GCGGTACTGCCATCGAGACACTGGCGCAGGCTATCGCACCCGTTATCGGCTACAAACAAATCGCGGTATGCGTTCTT
GAGCATGAGTCGGCGACCGTCTGTCATGGTCGACACCCACGACGGAAGACGCAGATCGCCGTCAAGCNTGTGTGCCGC
GGATTATCAGGACTGACCTCCTGGCTGACCGGCTGTTTGGTCNCGATGCCCTGGCGCCCGGCGGCGT

.....Rv303T7.seq:..... (SEQ ID NO. 379)
CATCACCTGGTTCATGAACTGGAAGCAGCGCAGCGCTTCCTTTTCGGCCGCAACATGAGCCAGCCTCTCGTCGGCGG
TCGGGTGCAGGTGCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCCTGAAACCAGCTTCCATATCCCGCGACGAACG
ACGCCAGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACANCGCGTTCTCCACCGACCGGCGCGGGTGTGG
GGTGT (SEQ ID NO. 380)

Clone Rv304

.....Rv304SP6.seq:.....
CTCAAGCTTCCCGGCGCCAGTACCGAAAGCGCGAAGCAGCTCGCGGCAGCCCAACNTGCTGCGTCGGATTGCCGGC
GGCGANATCAATTCCAGGCAGCTCCCGGACAATGCGGCTCTGCTGGCCGCAACGAAGGACTCGAGGTACCCCGGTG
CCCGGGGTCGTGGTGCACCTGCCGATCGCACAGGTTGGCCACAACCGGCGCTTGATGCCCGGTCGGCAAGCCCGGC
AGTTGCCAAACCCAGCGTATCAGGCTCGGCTCGCGAGTTGCGCGAAGAAGTGGCTCGCCTGATCACCTACCATCGGC
CAGGATCTGCGTGTATCACNACGCTCGCAAGGAGGTTGTTGTGGTGCT (SEQ ID NO. 381)

.....Rv304T7.seq:.....
GCCACGTTTCGCGCGCGCCGCGCATACGGCGGCGTACCGATCTCCGCTCATACACCCGCGGGTAATCGCCGACGGTGC
CGGTTTCGCGAGCCGAAGGTGACGACGCTGATTGAATCGAGTTCAGGTCAGCGGGTGGCGCAGCAACGGCGCGAGCT
CAACGACGTCAATCAGTTGTGCTTTCTACGGTCACCGACCCGGTGACCGTAGTCGCCCCGGTGCCTCGGCCGAGAA
GTTGCACCGCCACCAACCGGACACCGTCTTGACGCGGACGCCACCCCGGATCGGTTGTTGGCCAAGGTAATTGGGT
CATTCCATTGACGGGACGCCGACCCCGAGCCCCAGTACCGCCACGACCAGCGGCTGACCCACCACTGTACGA
ACACCAAGGCGACGCCGACCA (SEQ ID NO. 382)

Clone Rv306

.....Rv306SP6.seq:.....
CTCAAGCTTGTATGCCGCTAAACCGAAGCGTGAGCAGCGCCGCCACCCACCACGCGGGTTCGGGCGCCGGGCCCCGGGC
CGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCGCGAACCACCCGGCTGCGCTACGTCAAGCCATACCGGGCGGA
GCTACATCGGCTCGGCCGCCAGTGTTCGGGCCCTCTTTCGAGGTCNAGGTCNATACCGATTGCGCATCCGCGAGCCG
CACCCTGGACGACAGAACCCTGCCCTACGAGTGCTTGTGCGGCGGGGCCAAAGAACANCTTGGCATCTTGGCGCGATT
GGCCGGCGCGTCTGCTG (SEQ ID NO. 383)

.....Rv306T7.seq:.....
CTCGGTACGCTTCGGTTCGAGTGTGCGAGTGATAGATGACGACCGGGACCTCGTCGGCATCTTCCATAGCCCGCCAC
ACCTTCAGTTGCTCACCGGAATCCAACCGGTANAANGTCGGCGAGCGCTCGGCATTGGTCATCGGGATATGCCGCTCG
GGACGCTCAGAGCCCTCGGTCGCGCAGCACTCCGAGGCTTCGTGCGGGTGGTTCGCGACNCGCATGGGCCACCATC
GCATTACACAGGTCTGCGCG (SEQ ID NO. 384)

Clone Rv307

.....Rv307SP6.seq:.....
CTCAAGCTTCAATTCCTCCACGACGCGTTCCCAAATGAATTTCCCGATCCCACAATCTCGGTTTCAGATACAGGTCGCC
ATACCCCTTACTTCGGCAACGCTGGGCGGATTGGCCCTGCCGCTGCAGCAAACCATCGACGCCATCGAATTGCCGGCA
ATCTCGTTTCAGCCAATCCATACCCATCGACATTCCGCCGATCGACATCCCGCCTCCACTATCAACGGAATTTTCGATG
TCGGAGGTCGTGCCGATCGATNTNTCCGTCNACATTCCGGNGGTCAACATCACCGGCACCAAGNATCGACCCGATTCCG
CTGAACCTTCGACGTTCTCAGCAGCGCCGAACCA (SEQ ID NO. 385)

.....Rv307T7.seq:.....
TTAACCCCGTGGCCTCTACGCCGCTNCGGGTCGAACATGCATCCCGAGCANATGCTCGAGCGCGCACCCACTCGC
CGATGGCCGGAACCGGCTGGTTACCCGGGTGGCGGCTGACGTTTCGGCGGCGAGGACATCGGCTGGGAAGGGGCGCTTG
CCACCGTCGTGAAGACCCAGATTGAAGGTGTTTCGTGCTCTACGACATGACCCCGGCGGACGAGAAGAACCTTG
ACCGGTGGGAAGGCTCCGAGTTCGGCATCCACCANAAGATCCGATGCCGCGTT (SEQ ID NO. 386)

Clone Rv308

.....Rv308SP6.seq:.....
CTCAAGCTTGATTTTGATCATCATGGATGATCATACCCGAAGTGTGGTAGCCGAGTGGTTATCGTGGGTACCGTCG
TGCTTTCCATGGGCGCCTCTTTCGGGCTTTCGTTATGGTCTGGCAGGACATTCTGGGTATCGAGTTGTACTGGATGG
TGTTGGCGATGTCGGTGATCCTGCTCCTGGCGGTGGGATCCGACTACAATCTGCTGCTGATTTCCCGGTTGAAAAANG
AAATTGGGGCCGATTGAACACCCGAATTATCCGTGCCATGGCTGGTACCGGGGGAGTGGTGACGGCTGCCGGCATGG
TGTTCCCGGTTACCATGTCGTTGTTGTGTTTCAGCGATTTCGAATTATTGGTCAGAT (SEQ ID NO. 387)

.....Rv308T7.seq:.....
CGNCCAACCCGAATTGGTTTTTCGGCGCCNTCGGTGAGGACGGCGTGCGGGTGCTCAACGACGACGTCGTCCGCGGGAC
ACACCTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGTACAACGCCGCGCGGAACGCTTCCG
CCNCGGCGTTACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGACGGCATCGCCACCGGAGCGACGGC
CAAGGCGGCGTGCCAGGTGCCCCGGGCGCACGGTGCGGACAAGGTGGTGGTGGCGGTCCCGATCGGCCCANACGACAT
CGTGGCGAGATTGCGCCG (SEQ ID NO. 388)

Clone Rv309

.....Rv309SP6.seq:.....
CGTGACTGCCACCGGGGCCACTCCGCAGAATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTCGCCGA
CTTTCCGCGGTACCCGCTCAACTTTGTGTCNACCCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAATACTT
CATCCTGACGCCGGAACAAATTGACNCAGCGGTTCCNCTGACCAATACGGTCGGTCCCACGATGACCCANTACTACNT
CATTGCGACGGANAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGGT
TCAACCAAACCTTGAAGGTGATTGTTAACCTGGGG (SEQ ID NO. 389)

.....Rv309T7.seq:.....
TCGCTCAAGCGCNTGAGGCCGAANCGGCTGGTTACGACTCCCTGTTTGTGATGGACCACTTCTACCAACTGCCCATGT
TGGGGACGCCCCGACCGCGATGCTGGAGGCTACACGGCCCTTGGTGCGCTGGCCACGGCGACCGAGCGGCTGCAAC
TGGGCGCGTTGGTGACCGGCAATACCTACCGCAGCCCGACCCCTGCTGGCAAAGATCATCACCACGCTCGACGTGGTTA
GCGCCGGTCGAGCGATCCTCGGCATTGGAGCCGTTGGTTTGAGCTGGAACACCGCCAGCTCGGCTTCGAGTTTCGGCA
CTTTTCAGTGACCGGTTCAACCGGCTCGAAAAGGCGCTACANAT (SEQ ID NO. 390)

Clone Rv30

.....Rv30SP6.seq:.....
ATACTCAAGCTTCCGCTGGGGCCTGTCAACCATGGCGATCCCGTTGGTCCCGGACATCCCGAACGAGGACACCGCGA
CCCNCTTCGGTGTGTGATCATTACCGTTGGGCCACTGCGTAACCGCTTGGCGCACAAAGAGCCCGGTCTCGACGTCCG
AAAGCTCATCGGGCACCCGATTGAAATGCAGCAGCGGCGGCCACACCCCGTGCCGAGTGACAGAATTGCCTTGATCA
GCCCCAGGTTCCCGCCGATGCCGTGCTGTGCCCCATGTTGCTCTTGGCCGATCCAAGCGCGCAGGGGGTGGCCGCGC
CATAACCCGCGCCAGGCTGCGGTACTCAATCGGGTCGCCGATTGGCGTACCGGTGCCGTGCGCCTCCACCACACCGA
CCGTTTCGGGCTG (SEQ ID NO. 391)

.....Rv30T7PEG.seq:.....
CAACAGCGTTCCAGCGGCATACACCGCACATGCCGTGCACCCGGCGCCGGGCGGAGTCGCCGATAACACANGTACA
CCTTGGGAATCGGTGTGCGCCAGGGATTNACCGCGGGGTGGGGCCGGCGATCGCGCGCCAGGTTCGAGTTGGCGCCGA
CCGTGATNTACCGCCGACGTAGTTGGCGTTGTGGTCCGCCATCCGCGCGGCGGGCACGGCGCGGGCCGCCACCGA
TGTCACGGAAGCCGGGGGCGAACGCTCGACGACCTGGTTACCGTCTCNGTCGNTCNANCGTGGACCCGACNGCACGT

GGGCATATGTCCANAACGGACGNGGCCGGTTTCNTCGATGCNGCCGGGGTCCGCGACNTGCGGACNCNCNGNCACACC
ATCCGCCAGTCCGCGTGGCGTCCGCCCGGACTCTGCCTCGGCCCGGCCA (SEQ ID NO. 392)

Clone Rv310

.....Rv310SP6.seq:.....
CTCAAGCTTTGNCGACGATCGGGCGATGTGATGANAGGAAACCCAGCGCACAAACCGACNATTTTGGCGTAGCCGGC
GGACNTCTGCTCGATTCCGATCACGTGGCGCTCGCATCGAGCATGGCGCCGGCGACGGCTAGCAGCGATCCGCCGTC
GTCGAGGAACACGACACGAGCCGTACGCCCGGCCGTAAGCCGCGCCAGGATTCGGCGAAAAACCGTTCTACGTGGCG
GGTGTACTGGGTGTCCAATGATTCTGTGGGGTGCCTAGGCGTGCCTGCAATCTGCGACATAAATGCCGTCCGCCCGCAT
CCGCTCAACAACCTCCCGGGTGGTGAATANCACTTGCCGA (SEQ ID NO. 393)

.....Rv310T7.seq:.....
TCCAACGCGGTGACAGATTGTCTATCCTGGACCTGACGGTGAGGTGCAAGTTTTCAGGAATTCGGCAAAATCGGTA
AGAGCCTGAAGAATTCGGTATCGCCGGACGAAATCTGCGACGCATACGGGGCAGATACGCTTCGGGTTTACGAGATGT
CGATGGGGCCGCTGGAGGCTTCACTCCATGGGCCACAAAGGATGTTGTGGCGCGTACCGTTTCTGCGAGCGGGTGT
GGCGCTTGGTCTGTCGACGAGCACACCGGCCGAAACTCGGGTGGCTGACGGCGTGGAATCGACATCGATACGCTACGGG
CGTTGCACCGCACCATCGTCGGCGTGTG (SEQ ID NO. 394)

Clone Rv311

.....Rv311SP6.seq:.....
CTCGTCCTTGACTACGCCAGTATCGAAANCCTCCTGTGCCGGTNCGCTAAACACCCGGCGGACACTCANACGGTGCT
GGTGGTGCGGCATGGCACC CGCGGGCAGCAAAGCGCACTTCTCCGGGGACGACAGCAAGCGACCGCTAGACAAGAGGGG
TCGTGCGCAGGCAGAAGCGTTGGTACCACAGCTGCTGGCGTTCCGGCGCCACCGATGTTTATGCCCGCGACCGGGTGGC
CTGCCACCANACNATGGAGCCACTCGCCGCGGAACTGAACGTGACCATACACAACGAGCCNCCCTGACCGAAGAGTC
CTACGCCAACACCCCAACCGCGCCGACACCGAGTGCTGCAGATCTTCG (SEQ ID NO. 395)

.....Rv311T7.seq:.....
GTATCGCCTCCNCCCTTGGCCACCAGCAGCCACAGCGCGGTTCCGCGACCGAACGTGGACATCAATAGCCCGGAATCG
GTGTGTGCAAGTTGGTAAACGGTGTTGATCCCAAGCTTTGCCAGCCTTTTCGTAGTCTTGGGCCCCACACCCACAGT
GCTTCGACGGTACGGTACCCATGATGGCCATCCAGTTGGCATCGGTGAGCTGATAGATGCCAGCTGGTTTCGCCAAC
CCGGTAGCGATCTTGGCGCGCTGCTTGTGTCACCTGATACCTATCGAGCAAGACAGCCCGGTTTGGGACAAGATGACT
TTTCGGATCTCTTCNGCGAACTTCCAATGGGGGTCTCCGGGANT (SEQ ID NO. 396)

Clone Rv312

.....Rv312SP6.seq:.....
CTCAAGCTTTTGGTCTAGCCGGCCGAGCACGATACGGGTGTCTTGGCCACCGGCGGCGGCTGTCCGGGAAATGGCGG
GTCCCCGGTGGTTTGTGTGANGANTGCTGAACCGTAGTCAAGTGGGCGCGCTCAGACTCCACCCAGCCAGCAGGCAG
CGCGAAGCTGAATCCTCCAACCGGGTGTGATCCGGACAGGTTGGGGTGCCTTGGGGCAATGACAGGTGGCGGCGG
TGCGTTCCGGTCCGGCCGGCGGAGGTGCTGCGTTGGGATCNCCTGGCTGGGCATTCCGCNTNTTGGCGGCGGCGGTGG
TGGGGGGGCAACANGTGTCCCGGTGCGGGTGGCGCTGC (SEQ ID NO. 397)

.....Rv312T7.seq:.....
ATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTCCCGACTTTCGCGGTACCCGCTCAACTTTGTGT
CGACCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAATACTTCATCCTGACGCCGGAACAAATTGACGCAG
CGGTTCCGCTGACCAATACGGTCCGTCCACGATGACCCAGTACTACATCATTGCGACGGAGAACCTGCCGCTGCTAG
AGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGGTTCAACCAAACCTGAAGGTGATTGTTAACC
TGGGCTACGGCGACCCGGCCTATGGTTATTCGACCTCGCCGCC (SEQ ID NO. 398)

Clone Rv313

.....Rv313SP6.seq:.....
CTCAAGCTTGCAATGCGGGTCCGGATGCCATGGTTGGAANATGGTCCGCTGCGCTCNAATACGCGCGAGCGCATGA
GCTCACCGGTTCCGAACAACGTATCGAAAAACGTGCACTGCTGGCAGATGGTATCTCCGATGTGGTTGTAATTTGTA
TCCCAACTCTAACTGTGCTATCGGATCAGCGTGAATATCGANATATTGCGAATGCGATGACAGGCCGCCATTCCGGTTT
ATTGCTTACGCTTCCCGGGTTCGATTCGTCTGATGCACTGCCGCAAAACGCGGATATGATTGTTGAAACCGTATCTA
ACGCAATTATTGATGTGGTAGGCGGCAGCTGCCGTTTTGTGCTGTCGG (SEQ ID NO. 399)

.....Rv313T7.seq:.....
CAAATACACGCCGGACGCACAGCGGACATCGCCATCCCGAGCACACCCAAAACGGGATACAGGATGGAGGCCAACGC
CACGGCCGCGCCAGGATCACCACACACCGGCTTGGTCAGCTTGTGCGCGCGGTATAGGCATCGGGCCGCTGCAA
CGCAGCATGCACAAACGCGTACACCGCTGTACCAAGACGGCGACCAGCAATACCAGCATGACGGTACCCACGAGGTG
GCTCACGCATTACAGACTATGCGGTTTGCATCCAACACG (SEQ ID NO. 400)

Clone Rv314

.....Rv314SP6.seq:.....
CTCGTCCTTCGGCCTCGCTGCAGGAGTGGGAGCCGACGGGCTGGAAATCCGAAAAACGAGCCGGTGATCGCACTGTGCG
CCGATCGGCGCCGCACCTGGTTGGTTACGGATGAATCCGCAGCGAAATGTGGCTGCGGTGGCGTGTCTGACTCGT
TGGCGTCGACGCTGGTGGCAGCCACCGAGCGGTGGTCCAGGATCTGGATGGGCAAAGTTGTGCGGCCCGCGGTGA
CGGCCGATGAGCTGACCGAGTGCAGACGCCGTGTGGCTGACTTGAACCGACATGGAGTCGCCCCGGTT
(SEQ ID NO. 401)

.....Rv314T7.seq:.....
GTCTAGNCCGCCGAACACGATACGGGTGTCTTGGCCACCGGCGCGGCTGTCCGGGAAATGGCGGGTCCCGGGTGGT
TTTGTCTGAAGANTGCTGAACCGTAGTCGAAGTGGCGCGCGTCAAGTCCACCCAGCCAGGCGAGCGGAAGCTGAA
TCCTCCAACCGGTTGTGATCCGGACAGGTGGGGTGGCTTTGGGGCAATGACAGGTGGCGCGGTGCGTTCGGGTG
GGCCGGCGGAAGTGTGCGTTGGGATCGCCCCGGTGGGCATTCCGCGTGTGGCGGCGGCGGTGG
(SEQ ID NO. 402)

Clone Rv315

.....Rv315SP6.seq:.....
ACTCAAGCTTGAGATTGGCGTCAACGGGTGTGCGCACCGCGCTCCTGCAGTTGGTAGGCCTGCAGTTTGTGCATCAGG
CCGATGCCGCGGCCCTCGTGGCCACGCATGTACANACACCGCCGCGCCCTCACGGGCGACCATCGCCAGCGCGGCG
TCCAGCTGAGGCCCGCAATCGCAGCGGCGTGACCCAAACACATCGCCGGTCAAGCACTCCGAATGCACCCGGACAGC
ACGTCG
TCACCGTCGGCGTTGGGCCCGGCGATCTCGCCGCGGACCAGCGCGACATGTTCCACGTCTCTGTAATGCTGGTGTAN
CCGATGGCGCGAAACTCCCCATGACAANTCGGAATCCCGCGCCTCGGCGACCCCGCTCAATGTTGCTTCTCNTGCTTG
(SEQ ID NO. 403)

.....Rv315T7.seq:.....
TCGACNAGCATTCTTGACNGTTGTTTTGGCTCGGCATGGTTAGCCAAGGTTCTGCGGTCCCACCAGATCATCTTGGTC
CGGTAGCGCTCGTCCGGGTATGCTGCCGCGGGATTCTCGCTGCTATTACTCCCCCGAAGAACGCCACCGGTCCAGC
GCGTGGGCGCGCGGTTCCCATCACAACCTGAACCCCCAACAGGGGACATGCTTAGCGGTAGGGCGCGGCCAAGGC
GGCAGCAATCGCATCACTGCGCTGCGCGTCACTATTAACCCACCCGGACTTCACTTCCACGACCCCGAATGGCGCCCG
TGATTGATCATCTTGCGCACCGCGGATAATCCGGGAT
TG (SEQ ID NO. 404)

Clone Rv316

.....Rv316SP6.seq:.....
ACCGGGGCCACTCCGCACAATCTGTACCCGACCAANATCTACACCATCGAATACGACGGCGTCCGCGACTTTCGCGG
TACCCGCTCAACTTTGTGTCNACCCTCAACGCCATTTGCCGGCACCTACTACGTGCACTCCAACCTACTTCTGACG
CCGGAACAAATTGACGCNCGGTTCCGCTGACCAATACGGTCCGTCCACNATGACCCANTACTACATCATTCGCACG
GANAACCTGCCGCTGCTAAAGCCACTGCGATCGGTGCCGATCGTGGGAACCCACTGGCGAACCTGGTTCAACCAAAC
TTGAAGGTNATTGTTNACCTGGGCTACGGCGANCCGGCCTNTGGTTATTCCACCTNCCGCCCAATGTTTGCNACTCC
CGTTCGGGGTTGTTCCCNNAAGGTCAACCC (SEQ ID NO. 405)

.....Rv316T7.seq:.....
CGCTCAAGCGCNTGAGGCCGAANC GGCTGGTTACGACTCCCTGTTTGTGATGGACCACTTCTACCAACTGCCCATGTT
GGGGACGCCCGACCAGCCGATGCTGGAGGCCATACACGGCCCTTGGTGGCTGGCCACGGCGACCGAGCGGCTGCAACT
GGGCGCGTTGGTGACCGGCAATACCTACCGCAGCCCCGACCTGCTGGCAAAGATCATCACCAGCTCGACGTGGTTAG
CGCCGGTCGAGCGATCCTCGGCATTGGAGCCGGTTGGTTTGANCTGGAACACCGCCAGCTCGGCTTCGAGTTCGGCAC
TTTCACTGACCGGTTT (SEQ ID NO. 406)

Clone Rv317

.....Rv317SP6.seq:.....
CTCAAGCTTGCGTTCGATGAAGTAGTCGTGCGTCAGCGCCGCCTCTTCGAGCTCCTTGGCGATGCCAGCAAGGAGTC
ATCGCCGCGAGCTTGGCCAGGATCTTGTGCGCTGTTCTTGACGATGCGGGCCCGCGGATCGTAGTTCTTGTAGAC
ACGATGACCGAAACCATCAATTTGACCCCGGCTCGCGGTTCTTGACCTTGGCTACAACTCGCTGACGTGCTGCGC

GCTGTGCGGAATGCCCTCGAGCATCTCCAGGACAGCCTGATTGGCGCCGCCATGAAGCGGACCCCATAGTGCGTTGATGCC (SEQ ID NO. 407)

.....Rv317T7.seq:.....
GGTCAGGCCGAGCAGGCGCGAGGAACGACGAACCAACAAGCCATGGTGGTTGGCGCCGTCGAGAGGTCGGCGGTCGC
CACAACGGGAAGATCGCCTTGAGCGTCGCTCGACCGCCGCTCGAGTTGGGTCATAACGAAGTAGCTGATGCCGATCA
TGTCGACGTTTCCGTCGCATCAGCGTCGAGCGGCGACCCACTCNACGAGGTCTCGGTGCCGCGCGGCCAGGGCACCA
GCAGTGACGAGTCCAGGCGCCGTCGGGCCAAGCAGTCGCGGTGCCANCCGTGGTGGGTCGGGCGATGGTTGGGTGTGC
TCATTTCGGGAACGCCA (SEQ ID NO. 408)

Clone Rv318

.....Rv318SP6.seq:.....
CTCGAAGCTTTAACAGCATCAACCCCGCCCCGACCAGCACCGACACNATGTCGATGCCATCGAGGTGAATGTCGAAC
TGCGCGAAACCATCGGCGACCGCGACCACCGGCAACATGGGTACCGCGATTTCGGGTGCCAATGCCGACCCGACGGG
CCGCTCTCACCGCAGGTGACCTCGATCACCGAGACCANCCGGCCGTTNTNNTCACGCACCCCTACCGTGTACGCCCCA
AAACGGCGCTGGTGGTCGATTGCCGGAGTGCACCCCNACCCAGTGTGTCGCCGGATCC (SEQ ID NO. 409)

.....Rv318T7.seq:.....
TGATGCCGCACCCGATCGACGGTCGTTGGTCGGGGTTGACTGGCCGCCCCGGCGAAGCAGGGCGTCGACCGCGGCCCGG
ACGTGCGCGCGCGCTCACCGGTGCGCCATTGCCCGGGCGGGAGTCGTCGAGCTGACCACGGTAGACAAGTCGGCGCTGG
CCGTGGAAGACNAACGTGTCGGGTGTGACGGCCGCGGAGGAAGGCGCGGGCGACNTCTTGGGTTTCGTCGTANAGATAC
GGGAACGTCCAGCCGTGGCGGGCGGGCCTCGGCGACCATCTGATCGGGCCCGTCC (SEQ ID NO. 410)

Clone Rv319

.....Rv319SP6.seq:.....
TTTCGGGGCAGGCGGTATANCTTCCNCTCGTACCGGCGACCGCCAGCCGANAAGCTCGTTTTCCAGTGTTGCTGGGG
ATTCTCAGCTGCTGCTGANTGCGTGCCAAACCGCTTCCGCTTCGGGTACAAACGAGCCGCGGGGCTACNATCGTGCG
ACGCTGAAGTTGGTGTCTCCATGGACTTGGGGATGTGCCTGAACCGGTTACCTACNACTCCAAGCTGGCGCCGTCT
CGTCCGCAAGTCTGTGCTTGCATAGCCGGGAGGCGCGGATCCGCAATGACGGATTCCNTGCCANCGCTCCGAGTTGC
NTGCGGATCGACTACNAATTGATCACCCANAACCATCGGGCGTNTTACTGCCTGAAGTACCTGGTGCGGGTCGGATAC
TGCTATCCGGCGGTGACAACCCCGGCAAGC (SEQ ID NO. 411)

.....Rv319T7.seq:.....
GTTTTGGCTCGGCATGGTTAGCCAAGGTTCTGCGGTCCACCAGATCATCTTGGTCCGGTAGCGCTCGTCCGGGTATG
CTGCCGCGGGGATTCTCGCTGCTATTACTCCCCGAAGAAGCCACCGGTCCAGCGCTGGGCCGCCGCGGTCCCCA
TCACAAACTGAACCCCCAACAGGGACATGCTTAGCGGTAGGGCGCGGCCAAGGCGGCAGCAATCGCATCACTGCGCT
GCGCGTCACTATTAACCCACCCGGACTTCACTTCCACGACCCGAATGGCGCCCGGTCAATTGATCATCTTGCGCACCG
CGGATAATCCGGGATTGCCAGCCATTCTACTACCGCATGCGAGTCATCGGCTGACCGCAGCGGTC

(SEQ ID NO. 412)

Clone Rv31

.....Rv31SP6.seq:.....
TCGCCTAGGCGGGCTTCCCCTTCCGTCCGAGCNGTCAGAAGCTCCTATGACAATGCACTACCCGAGACNATCAACGGC
CTATGCAATACCNAGCTGATCAAACCCGGCAAGCCCTGGCGGTCCATCGAGGATGTCGAGTTGGCCACCGCGCGCTGG
GTCGACTGGTTCAACCATCGCCGCTCTACCGGTACTGCGGCGACATCCCGCCGGTCTAATCGACGCCGCTCACTA
CGCTCAACGCCAGAGACCANCCGCGGTGACGTCTCAGATCAGAGAGTCTCCGGACTCACCGGGCGGTTTCATCCCC
ACTGTCGATAGCGTCTGTGGATAACTTTGTCTGCA (SEQ ID NO. 413)

.....Rv31T7.seq:.....
GCGCGTNGAACTGATAGGTGCGGCCCGGCTCGAGCANGCCGGCCATTGTTTCGATGCGGTTACCGAAGATCTCTTCGG
TGACCTGCCCGCCGCGGCCAGCTCGGCCAGTGCCCGGCGTTGGCCGCCGCGGCGACAATCTTGCGTCCACGGTGG
TCTGGGTCA (SEQ ID NO. 414)

Clone Rv321

.....Rv321SP6.seq:.....
CTCAAGCTTCAATACAGAGTTATAAACTGTGATAATCAACCCTCATCAATGATGACNAACTAACCCCGATATCAGGT
CACATGACGAAGGGAAAGAGAAGGAAATCAACTGTGACAACTGCCCTCAAATTTGGCTTCTTAAAAATTACAGTTC
AAAAAGTATGAGAAAATCCATGCAGGCTGAAGGAAACAGCAATAACTGTGACAAATTACCCTCAGTAGGTGAGAACAA

ATGTGACGGAACCACTCTCAAATCTGTGACAGATAACCTCAGACTATCCTGTCGTCATGGAAGTGATATCGCGGAAGG
AAAAAT (SEQ ID NO. 415)

Clone Rv322

.....Rv322SP6.seq:.....
CTCAAGCTTCGATCGACATTACTCCCGCCTTGGGTCTGGTCTCCGAGCTGGTCGGTCATGGTCGGACCTGCTGGTAGT
GGGGATCTAACGCAACATGGTCGGGATTATCATGGTGTACCCGTGATACCCATTTCGAGCTGCCGGTGAAACCCCGC
GATGCCGGGATTTCCAGCCGCACTAGGATGTCTAGCCGGCCAGCCGCTGCCGCCGGAATTCCGGATGTTCCGGTATACC
ANCGATCGGCAATCTTGCGTATCCGCCGATGCTCGAACGCTANCCACGCCAAACCAACCACTGTGACNACAATCGCCA
CCACACCAAAGGTCATGCCCTCGGCGTGATGTCCGGTGCCGAAAGCCGCAAGAGCTCCGACGCCGCC
(SEQ ID NO. 416)

.....Rv322T7.seq:.....
CATTCCCAATTGAATTTCCCNATCCCAATCTCGGTTAGATACAGGTCGCCATACCCCTTACTTCGGCAACGCTGG
GCGGATTGGCCCTGCCGCTGAGCANACCATCGACGCCATCGAATTGCCGCAATCTCGTTAGCCAATCCATACCCA
TCGACATTCCGCCGATCGACATCCCGGCCCTCCACTATCAACGGAATTTTCGATGTGGAGGTCGTGCCGATCGATGTGT
CCGTTCGACATTCCGGCGGTCAACATCACCGGCACCAAGGATCGACCCGATTCCGCTGAATTTCGACGTTCTCAGCAGCG
CCGGACCCATCAACATCTCGATCATCGACATTCGGGCGCTGCCGGGCTTTGGCAACTCGACCGAGCTGCCGTCGTCCG
GCTTCTTCAACACCGGCGGCGGTGGCGGCT (SEQ ID NO. 417)

Clone Rv327

.....Rv327SP6.seq:.....
CTCAAGCTTTTCGGCGGAGACGGACANNTGCGAACATTGATGACAAAATAGAAATCATTGATGGTTTGAGTCACCAGG
CCGATCAAGCCTTCGCCGAGCCAAATCCAATCAAGAGGCCCAAGCCCGTACCAATCAGCCCGGCAACGAGGGATTCC
GTCATTATCAGCCAAAATAACTGCTCTCGGGTTACACCCAAACAGCGCAATATGGCGAAAAACGGTCGCCGTTGCACG
ACATTAAATGTCACGGTATTG (SEQ ID NO. 418)

.....Rv327T7.seq:.....
AGCTTAACTGCTCCCTAATACTGGGGCTGTGCTGCGGTGTATGCACGGCATAACGGACATCCNTCCCCTGAGACCCN
CGGTCTAATCAGCCACGTGTCCACCATCAGGGGTCAACCCCGGCCAAGGGCGACGGCACCCCAAGTTCCGCCACCGTT
AACCTATTGCTGTGAGCTTCATTTGCTGCGAGCAAAACAGTTGGTCGGCCGTTAGGAACTGAATTGACACTCAACCGA
TTTGGTGCCNCCGTAGGTGTCTGGCTGCGGGTGCGTGGTGTGTCCGCGTGTGGTAACGACCACAATGTGACCGGG
GGAGGTGCAACCACTGGCCACGCGTCCGCGAATGTCTATTGCGGGGG (SEQ ID NO. 419)

Clone Rv328

.....Rv328SP6.seq:.....
CTCAAGCTTGGGGTGGCGCTGTGCGTGGTGTGCTTGGCGGCGTGGTATCAACACCGCCACGAAATGGGGCACAAG
AAGGATTTCGTGGAGCGGTGGCTGTCCAAAATCACCTCGCCCCAGACCTGCTACGGGCACTTCTACATCGAGCACAAC
CGTGGCCATCACGTCCGGGTGTCCACACCGGAGGACCCGGCGTCCGGCGGTTCCGGCGAAACGTTGTGGGAGTTCTTG
CCCCGAGTGTATCGGCGGCTTGCCTCGGCCGTTTATTGGAGGCCAACGGCTGCGTCCGGCTCGGCGTCAGCCCC
CT (SEQ ID NO. 420)

.....Rv328T7.seq:.....
GCACCAAGGCCCCACACGTCAACCTGTGACCTCCTGCGCCGACCCCGCCGAGGTCCTGGCCGTTACCACCTGAACGG
GCGAGCCGGGAGTCTGGTACGCATCGAACAAAGAGCAAGGTGCATGGGCGGAGTTGTTCCGCCACTTCGTTCGATGACG
GGGTCNATCCATTGAGGTCCGTGCGCGGTCGGTCGAGTGGCGGTCACACTCCAGGTACTCGACCTCACAGACGAGA
GGACTCGATCCCATCTAGGTGTGGACGAAACAGATCTTCTGTCCGA (SEQ ID NO. 421)

Clone Rv329

.....Rv329SP6.seq:.....
TCGCCTCCGCATATGGGTCGACGCCAAGCGGGTCCGGATTTCTGGGCTTCATCGCTCGCGCCGTCGCGACAAACAGCG
CGTCCGAACCGACACTCGTTGTGATGTCCAGCTATCACCTTCGGTACGCACCCAATCGACCTACNCGGCTATCTCA
GCCGCGATCTCCAGGTCCGCGGAGCCAGGTGCATCCCGGTCCGGATCCCACTAACCCGGCACCAATTGGCGTCN
(SEQ ID NO. 422)

.....Rv329T7.seq:.....
GTCCTCGAGTGCCGCCGTCGNACNCCCAGCGCCCGCGCGGCCACTTGGATGCGACCCGTTTCAAGTCCCTTCATCAT
CTGCGAAAAGCCTTGACCATGGCTCCGCCCAGGATCGCCGAGACCGGCACCCGGAGGTTGTCGAACGACAGCTCGCA
GGATTTCGACGCCCTTGTAAACCAACTTCGGCAAGTCCCGGACACCGTGAGTCCCGGCCCGGGTTCGACGAGCACGAT
CGACATGCCTTGGTGCCGCGGTGTGGCGTTTCGGGTCGG (SEQ ID NO. 423)

Clone Rv32

.....Rv32SP6.seq:.....
GGCATACCAATGTGGACTTCTGCTCACCACGATATCCGTGGTCTGATCCGCTGCTGCGGCGGGGCTGCNACCTGCNTC
TCNGCGGCACCCGTNACTACATGGCNCGCGCCGACGATACGTCGCGGCGGGGACCCACTCCNACTGGTCGACGGTGC
TGGCCGCGTGTCCGCANGTCCCNAACCCGCGCCGACCGACGAAACCGGCGCGCTCCGTCTGGACCAACGCTCATGT
GCCGTGCGGGTCCATGCTCGACGCCATCGAGACCGTAACCAGCGTCCTCGAGCGGTTCCGCTCCGGCTTCCGTGACAT
CTTCGTGGTGTGCTCGCGCGGTGCCGCGCGCGGATGGTCGACCACAACGCCAACCACTCGGCGGTGACATCACCGTC
CGCGCCACTCGACCTGGCGCGCGATCGCGGCC (SEQ ID NO. 424)

.....Rv32T7.seq:.....
GTGAGCAGACCTACGCCNCTGGTTGCGCCAACTCGGTACCGATCATGGCGCGCNGCCTGTGCTCACCAGATACCCAGC
GAACAAGACAGCCCGGTCCGCGACAAGATGACTTTCGCGATCTCTTCGCGGACTTCCATGGGGTGTCCGGAGTCCCG
GGCGCCACCGCGAGGTAACCTCGTCTCAGTCCCATACGCGACCGGGTATCCACGTGCGCGCAACAACGCCACCACTC
CCCAGACGCCNCGTTGTACGCGGCTGGGTTCCACNGCAATAAGTGGCCTCANGGCATCGTCCGGCGCGGTCCNCAAC
GCA (SEQ ID NO. 425)

Clone Rv330

.....Rv330SP6.seq:.....
CTCAAGCTTGAGGTTAACTTTGAACGGATCGAGCTGGACGTTTCGAGACGGTGATCGGGCCGAACCTGAATTGTCCGGT
AATGCCCAACGCAAAAAGCAGGTGGTGGCCGGGGCGGTGAAACCGGCGTCGGCGGCACCGTCGAAATCTATGTGGAT
TGCCGGAAATGGGGATGTCCGGCACGGCGAAACCGTAGTTGCTTGTCCCGTGAGGCCCAGGTGGATGGGGGAAAGAT
CCTGGTGTCCGGGATAATAATGGGGCCGATGCCGCGGTTGAAGTCCACTGGATCGGGAATCCGGAATCTTGATCCG
ACGTTACAGCCGAACAGGCCCTC (SEQ ID NO. 426)

.....Rv330T7.seq:.....
CGGCGACGTGCGGATACGCCGAGCAGTTGGGAATCGCTCTGCAGCAAACCAATATTCTGCGCGACGTTTCGAGAGGACT
TTTTGAATGGACGGATCTACCTGCCGCGCGACGAGCTGGACCGATTAGGCGTACGCCTCCGCTGGACGACACCGGGG
CACTCGATGACCCCGACGGACGGCTCGCGGCNCTGCTGCGGTTCAAGTCCGACCGCGCGCGAGACTGGTNTTCGCTGG
GACTGCGGCTGATTCCACACCTCGACCGCGCGAGCGCTGCCTGCTGTGCGGCCATGTCTGGCATCTACCGCGCTCAGC
TCGCTTGATCAGAGCATCGCCGCGGTCTGCTA (SEQ ID NO. 427)

Clone Rv331

.....Rv331SP6.seq:.....
CTATAAAATACTCAAGCTTGATGCCGCCGAACCCGAGCGTGAGCACGCCGCCAGCCACCACGCGCGGGTGGGGCGCCG
GGCCCGGGCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCGCGACACCACCGGNTGCGCTACGTCNAGCCATA
CCGGGCGGAGCTACATCGGCTCGGCCGCCAGTGTTCGGGCCCTCTTCGAGGTCNAGGTCNATACCGATTGCGCAT
CCGCAGCCGCACCTGAACNACANAACCGTGCCCTACTATTGCTTGTGNGCGGGGCCAAAAACAGCTTGGCATCCT
GGCCNATTGGCCGGCGCGG (SEQ ID NO. 428)

.....Rv331T7.seq:.....
CTTCGTGCGAGTGTGCGAGTGATAGATGACGACCGGGACCTCGTCGGCATCTTCCATAGCCCGCCACACCTTCAGTT
GCTCACCGGAATCCAACCGGTAGAAGGTGCGCGAGCGCTCGGCATTGGTCATCGGGATATGCCGCTCGGGACGGTCAG
AGCCCTCGGGTCCGGCCAGCACTCCGCAGGCTTCGTGCGGGTGGTCGCGACGCGCATGGGCCACCATCGCATTACCA
GGTCTGCGCGAATCNCCANCACGTANACNGTTCCTTCTAA (SEQ ID NO. 429)

Clone Rv333

.....Rv333SP6.seq:.....
CTGGCACCAAGGCCCCACACGTCACCCTGTGACCTCCTGCGCCGACCCCGCCGAGGTCTTGCCGTTACCAACCGAAC
GGGCGAGCCGGGAGTCTGGTNCGCATCGAACAAANAGCAAGGTGCATGGGCGGAGTTGTTCGCCACTTCGTGATGA
CGGGGTCNATCCATTGAGGTCGCGCGCTCGGTCNAGTGGCGGTACACTCCAGGTACTCGACCTCACAGACNA
AAGGACTCNATCCCATCTAGGTGTGGACNAAACAGATCTTCTGTCGACNACTACACCACCAACCCAGGCCATCGCCGC
CGCCCGGATGCCAACTTCGACGCGGTAAGTGGCCCGCGGGGGCGCTCCCGGTTGTCAACACTTGGCGTGTTCNT
TCACGCNCTGCCCCACATCCAACCCAACG (SEQ ID NO. 430)

Clone Rv334

.....Rv334T7.seq:.....
GTTCTTGGGCCCCATGCGGAGGTATCGCCGTTTCCACCACGCGGTGCGGGTGGCGTTGCATTAGCTCACCGATGGTGGC
CTTGTGAGGCGCGGGGATACCCGAGTGCCGGTAAACCATCTTGTGCTGC (SEQ ID NO. 431)

Clone Rv335

:::Rv335SP6.seq:::

CAATACTCAAGCTTGGCGTGGCGTTCCAACCCGAATTGGCTTTCGGCGCCATCGGTGAGGACGGCGTGCGGGTGCTCA
ACNACNACGTGTCGCGGGGACACACCTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTAC
AACGCCGCGGGAACGCTTCGCGCGGGCGTGACCGCATCCCCTTGACCGGGCGGATC (SEQ ID NO. 432)

:::Rv335T7.seq:::

CNTCATGATGATCATCACCCGAAGTGTGGTAGCCGAGTGGTTATCGTGGGTACCGTCGTGCTTTCATGGGCGCCTC
TTTCGGGCTTTCGCTATTGGTCTGGCAGGACATTCTGGGTATCGAGTTGTACTGGATGGTGTGGCGATGTCGGTGAT
CCTGCTCCTGGCGGTGGGATCCGACTACAATCTGCTGCTGATTTCCCGGTTGAAAGAGGAAATTGGGGCCGGATTGAA
CACCGGAATTATCCGTGCCATGGCTGGTACCGGGGAGTGGTGACGGCTGCCGGCATGGTGTTCGCCGTTACCATGTC
GTTGTTTGTGTTACCGATTTGCGAATTATTGGTCAGATCGGTACCAC (SEQ ID NO. 433)

Clone Rv336

:::Rv336SP6.seq:::

ATACTCAAGCTTTACGGTGATCGNCATCACCTGGTTCATGAAGTGAAGCAGCGCAGCGCTTCCTTTTCGGCCGCA
ACATGAGCCAGCCTCTCGTCGGCGGTGCGGGTGCAGGTGCTCGGGCAGCTCGGCCGNACAGCCGCTGACCTGAAAC
CAGCTTCCATATCCCGGANNAACGACGCCAGTCCGCTACGTNACCCCTCCCGACTGTCCATGGACAACAGCGCGTT
CTCCACCGACCGGGCCCGGTGTGGGGTNTT (SEQ ID NO. 434)

:::Rv336T7.seq:::

GCTGGTAGAGTCGCTGACCGGTGCAGGTTTCGACAATGTGGTGCCGGTTCGGCGGCTACGTGCCATCGAGACACTGGC
GCAGGCTATCGCACCCGTTATCGGCTACGAGCAATCGCGGTATGCGTTCCTGAGCATGAGTCGGCGACCGTCGTCAT
GGTCGACACCCACGACGGAAGACGAGATCGCGTCAAGCATGTGTGCCGCGGATTATCAGGACTGACCTCCTGGCT
GACCGGCATGTTTGGTCGCGATGCCTGGCG (SEQ ID NO. 435)

Clone Rv337

:::Rv337SP6.seq:::

GCTTTCGCGGATACCCGCCATGTCNCGCACATCCAGGACTTCTGGGGGGATCCGCTGACAGCGGCGGGATCCCAAAG
TCCGGATGATCGGGCCGCTACGTCGTGGTGACCTCGTCGGTAACAACGAAACCGAAGCGTATGACTCGGTCCACGC
GGTGCGGCACATGGTGGACACACCGCCACCGCACGGGGTGAGGCCCTATGTACCCGGTCCGGCANCACTCAATGC
CGACCAGGCCGAGGCCGANACAAAANTATCGCTAAGGTCACCGCATCACNAGCATGGTGATCGCAGCAATGTTGCT
AGTGATCTATCGCTCCGTAATTA (SEQ ID NO. 436)

:::Rv337T7.seq:::

CTTCCAACCCGAATTGGCTTTCGGCGCCATCGGTGAGGACGGCGTGCGGGTGCTCAACGACGACGTCGTCCGCGGGAC
ACACCTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTACAACGCCGCGGGAACGCTTCCG
CCGCGGGCGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGACGCGCATCGCCACCGGAGCGAGGGC
CAAGGCGGCGTGCCANGTCGCCCCGGCGCACGGTGCGGACAAGGTGGTGCTGGCGGTCCCGATCGGCCCA

(SEQ ID NO. 437)

Clone Rv338

:::Rv338SP6.seq:::

TACTCAAGCTTCGCGAGATCCGGATGGCACTCACGCTGGACAAGACCTTCACAAAATCTGAAATCCTGACCCGATACT
TGAACCTGGTCTCGTTCGGCAATAACTCGTTCGGCGTGACGAGCGCGGCAACGCTNCTTCGGCATCAACGCGTCCG
ANCTGAATTGGCAGCAAGCGGCGCTGCTGGCCGGCATGGTGCAATCNACCAGCACGCTCAACCCGTA

(SEQ ID NO. 438)

:::Rv338T7.seq:::

CCCACGACTTCTCCTCGATCAGTTGGATTTGTACGAAGAGGCAACGAAAGCAGTGATCCTCGGGATGGTTCGACGCTT
ACATCGACCCGCGGTTACGCCGCACAGCCTGTAGATGCGCTGGGCGAGCAGGTCCACAGTTTCGCCGCTAAGGCAC
GGCGTCTGTTCCCGTCCGGATCGCCATTGCGCCTCGGCGTCTGCTCCCATTCGATCAATAGGGCTGGCAGCTCCGTC
GGCAGGGGCTACGCCTACCCCGTCACG (SEQ ID NO. 439)

Clone Rv339

:::Rv339SP6.seq:::

CTCAAGCTTATGCGCGCCGGCCGAGGTCTGCTCAGGCAACCCCTGAAGTTTAGGGGACNACCTACTCAGCGCAAAAT
TTCGCTAATGTGAGTCCGCCCCACAGGGGNANATCAACCCATGTCGATCATGATCTACCCGGATACGGGATTGGCGG
TAGCGCCACGATCGTCNAAATNTCCGCTGAATCATCGGATAGCTGATCCGGCGTCAACGCGTTTTGANTTCACCGC
GCAACAGCCGCCAGGCCGGCCGCANCGANCCGATCTCNTCGGGCCGCATGGGCCCAATCTTNTCG

(SEQ ID NO. 440)

.....Rv339T7.seq:.....

GTGTGTGGTGGAACCCATCTGAGCAGTGTGCCAAACCGGGCAGACAGCTCCCAATTGACGTGAGCCCCTCACTTGC
TGGGTAAGCGTC (SEQ ID NO. 441)

Clone Rv33

.....Rv33SP6.seq:.....

CTTTACACTTCCTGCATCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATG
ACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGGGCGTGACGGCCACCGGGGCCACTCCG
CACCATCTGTACCCGACCAAGATCTAC (SEQ ID NO. 442)

.....Rv33T7.seq:.....

CAGGCATGCAAGCTTTAGCTGCCC GAATGCGTCACCCCGATGCGCCAGATCGGGGCTTCGCAGATAAAGCACGAACA
GGCGGGCAAACGTCNATCTCGGAGCCGGAAGGGCAATCAGCCGACCGTCGACGAACGACACCGGGCAGACCACTTAG
GCAGTGACGGCCGGCCGAACATTACGCGCTCGTTGATTAGGCGTTCCGGTCTCGTCCGCGTCATGCCGAGCAGCTTG
CGGCAGATCTGAACGCTGTCTGTCCGGGCAGCGCGCCGGGCGTTGGGGTGCCTGCCCGAATGTGACGAAACGGAGC
CGGACCCGCTCTCGGCGGGCCGCGGACGGCGATCCGC (SEQ ID NO. 443)

Clone Rv340

.....Rv340SP6.seq:.....

CNCAAGCTTGCGGATGTTACCCCTGACAGCCTGAAGTATGTCNAAACACACGGCACCGGAACGGTGTGGGGGACCCC
ATCGANTTCGAGTCGCTGGCGGCCACTTATGGCCTGGGTAAAGGCCAGGGCNANAGCCCGTGCGCATTGGGGTGGTTC
AAAACCAACATCGGCCACCTGGAGGGCGGCCCGCGGTGTGGCTGGATNCATCAAGGCGGTGCTGGCGGTGCAACGTGGG
CACATTCGCCCGCAACTTGCACTTCACCCGGTGAACCCGGCCATCNACGCGTCGGCNACGCGGTGTTCTGTGCCNACC
NAAAACCCCCCGTGCGCGGGC (SEQ ID NO. 444)

.....Rv340T7.seq:.....

GGAACCGGTAACCAGATCAGCTCGTCGACCTCACTGCCGGGGTGAATTCCCCACCGGTGCTGCGCGCTGCCAGTAG
TGCACCTTCTTGACGCTCGAAAAGGGGAGTCGGTCGGGTAGGTCAACGTGAGGAGCCGCTACCCAGGTTGGCGCNA
TAGCCGGTCTCCTCGAGTATCTCCCGCACCGCCCCACCGGTGCGGTCTCACCCANATCCACTTTGCCCTTGGGCAGC
GACCAGTCGTCGTANCGGGGCGGTGAATGACAACGATCTCGACCGGCCCTTCN (SEQ ID NO. 445)

Clone Rv341

.....Rv341SP6.seq:.....

TACTCAAGCTTCAGAACAGGCCTGTTGTGGGCNACCCGGCTCGCCGAGTTCTGCACGCACCGCTCAAGTGCGGCC
GCACCGCCGGCATCTCCCGGTACGCGAGGGCCGCGGCCCGCGCCGAGCGACGGCGTGTTCGCGCAGTTGCCCGTCAA
TGATGCTGACCTGATCGGCCACCCGGGCGTTCTCGGCGTCTGCGGTTCACTAATCGCGGTGCTCAGCAGCGTCTCGA
CAGCCACCACCGAGTGCGGACCACTGC (SEQ ID NO. 446)

.....Rv341T7.seq:.....

TAATGTCTTGCCAACGTCACCACAATCGCGATGAATTCAATCATGCCGCCAGGGCGGCCAACCAATGGTGGCCGCG
AGCGGCAGCTCGATCGCAGCGCGGAGGTTGCCGGCCGCCAGTTGATTACGAACAGGGTGAGGTCATAGGCGGGCAGG
ATAGTGACGAAGGCAAGACCTATATCTGCCGTGGAAGAAGATCGAGTAGCCGGTCGACACAACGGAAGCGAAAGTG
TCCGCGATGTTGATGAGCGTCGCCGGTTGTGGCGCGGTGGCGGC (SEQ ID NO. 447)

Clone Rv343

.....Rv343SP6.seq:.....

TACTCAAGCTTTCGTGAGTTTCATCGCGCCAGCAGACCAACAAGAGCATCGGGACATACGGAGTCAACTACCGGCCAA
CGGTGATTTCTTGCCCGCCGCTGACGGCGCGAACGACGCCAGCGACCACTTACGANATGGCCAGCGCGTGGCGGGC
CAGCAGGTTGGTGCTCGGCGGCTACTCCAGGGTGCGGCCGTGATCGACATCGTCACCGCGCACCACTGCCCGGCCCT
CGGGTTACGCAGCCGTTGCCGCCCGCAGCGGANNATCACATCGCCGCGATCGCCCTGTT (SEQ ID NO. 448)

.....Rv343T7.seq:.....

CCACCCGTGAATTTGGGATGGGCNAAAAGGCNAAGCACCGCGTGGCCACGAACGCCGGGAGGGACAATCTCGGGCGG
CTAGGGCTTCTCGCGGGAAGGCCCGAACGTACGGCGTTTCAACACGTGCGGTGCGCCCTCGGACCGCGAACATTCGGGG
ATGGCAGCAACCTGGTAGCACCTGGCCGGGCGATGATCTGCAGCGTCGCCGCGGGTAGTCGCCGCCCGGGCGGCTAC
AGTCTGAAACGCGATGACCATCGATGTGTGGATGCAGCATCCGACG (SEQ ID NO. 449)

Clone Rv344

.....Rv344SP6.seq:.....
TCAAGCTTTAGCTGCCGAATCCGTCANCCCGATGCNCCCAGATCGGGGCTTCGCANATAAAGCACNAACAGGCGGGC
AAAACGTCNATCTCGGAGCCGGAAGGGCAATCANCCGACCGTCNACAAACGACACCGGCGANACCATTAGGCACTGA
CGGCCGGCCGAACATTACNCGCTCGTTGATTAGGCGTTCCGCTCTCGTCCGCGGTATGCCGAGCAGCTTGCGGCANA
TCTGAACGCTGTCTGTCCGGGCAGCGGCGCCGGCGTTGGGGTGCCTGCGGAATGTGACNAAACGGAGCCGGACCCN
TCTCGGCG (SEQ ID NO. 450)

.....Rv344T7.seq:.....

CCGGGGCCACTCCGCACAATCNGTACCNNACCAANATCTACACCATCGAATACGACGGCGTCGCCGANTTTCCGCGGT
ACCCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAATACTTTCATCTGACGC
CGGAACAAATNGACGCNTCGGTTCCGCTGACCAATACGGTCCGTCCC (SEQ ID NO. 451)

Clone Rv346

.....Rv346SP6.seq:.....
NCTGGCCTTTGGTCCACACTAANACAATACTCAAGCTTCCGGCCGAGAGCCGCCAACTCAGCATATCGTTAACCAGT
ATCCCGAGCCGATAGCTGGCGGGCTCGGGTGGTGGCCAGCGGCGTGCACNAAAGGTGTGACCGTCATGAAACAGAC
ACCACGGCGGGCGTCCGGCGTGTACCTGCTCGANATCTCAGCATCCGACGCGGTGTGATCGCGCTTTCCGGCGT
TNGTGGGTGNCCGCCGAGCCCGGCAAGGCCGGCCGACACAACCCCGAAC (SEQ ID NO. 452)

.....Rv346T7.seq:.....

CATCTGCCACCACACGACCGCGGTGCGGACGCGGCTGACGCGCTGGTGGTCAGCATCGTGGCGGCTGTGCTGTTG
TATGCCAGCTTCCCGCCGCGCAACTGCTGGTGGGCGGCGGTGGTTCGCTCGCATGCTGGCCTGGGTGCTGACCCAC
CGCGCGACGACACCGGTGGGTGGGCTGGGCTACGGCCTGCTATTCCGGCCTGGTGTCTACGTCTCGTTGTTGCCGTGG
ATCGGCGAGCTGGTGGGCCCCGGGCCCTGGTTGGCACT (SEQ ID NO. 453)

Clone Rv347

.....Rv347SP6.seq:.....
GACAATACTCAAGCTTGACTGGCCACCCACCGCATGACCACCGACAGGCCCGACTGGTCTGTAACCTCGAACGCCGG
GGTGTGATGTCCCAGCCGCTGAANTCGTCTGCGCGCGCAGGCCGTCNAACAGGTACAGGGCGGGCGAATTGGCACC
ACCACTTTGGAATTGGACCTTGATGTACGGGCCATCGACGGCGACGGCACCTGCAGGTACTCCACCGGCAAGCCCCG
CCGGGAAAATGCCCGCGGTNCCGTGCCACCGACGGCGCCGANCAAACCCGACACTAGGGCCGCGCCNACGGCCCC
GACCACNANTCNACGCGACATACCGTGACGGCGCCACNAACCCTGTCAACA (SEQ ID NO. 454)

.....Rv347T7.seq:.....

CCTCCAATCGGCGGGAAGCGACNCCAGCCTACCGAGCTTGGAGTCCANGACGCCAGCGGCGGCTCGGTCTGCGTC
GTGGTGCCGCGGGGTGGCGTTGGCTGGCAACGATCTCCACCCAGCCGGTCCGGTTACCCACGATCTCGGCATANACG
CGGGCCGAGGCCGGTGCATACCGTATTGCGTCAATTGGGACGCGGTTGTGATTGCGGTAGCTCGGTTGCCACACCC
GTCAGGGGTTGACGTTGGCGGTTCCGGCGGCCCCANACCGCTGTACCATGCCCGCAAGCCGACCTGCGGCGCC
ACCAACTGCAGCACCANCATGTCGCCGTGCGCGCCGCGATCACATGG (SEQ ID NO. 455)

Clone Rv348

.....Rv348SP6.seq:.....
CTCAAGCTTTTGGAGCTGCGCGGGGCANCTTCGCCGGAATTCTACTANCGAGAANTCTGGCCGATACGGATCTG
ACCGAANTCGCTGCGGTGCANCCACCCTCATTGGCGATGGCGCCGACNATGGCGCCTGGACCGATCTTGTGCCGCTT
GCCGACGGCGACGCGGTAGTGGTCAAGTCCGGTCTACGCTTGGGCCTTTCGGGACGGTCCCGACGCTGGTTCGGGTT
GCGCCGCNAAAGCGGCGGGTCCGGTGCATCAGGAATGCCTCNCCGCCGCGGCACTGCACGGCCAGTGCCGCGGCGA
(SEQ ID NO. 456)

.....Rv348T7.seq:.....

CNCCAGCTTGATTGGTCTGGTTCATTGGCCAGCTGCGCGAGCCTGGCTCACTTCAACTACGACGACCGCAAACAATT
GCCGCTTTCGGATCCGAGTTTCGGTTGGGTACGCGGCAATGGAGCACCATTCTCGGTGAATCAGACTATTCTGAGTA
CTTGATCATCCACTCTGCACACGACCTGCGAACCCCGCGCGGCTTTCGGACCTGGAGCAGCTGGCGCAACGTGTGAG
CCAGATCCCAGGCGTTGCCATGGTTCGCGGTGTGACCCGGCCAAACGGGGAAAC (SEQ ID NO. 457)

Clone Rv349

.....Rv349SP6.seq:.....
CAATACTCAAGCTTGACTGGGCGCGCACCTTCGGCGCCACCCACACCGTCAACGCCCGCGAAGTCNACGTCGTCCAGG
CCATCGGCGGCTCACGGATGGATTGCGCGCGGACGTGGTGTGACGCGCGTCCGGCGACCGGAAACCTACCAGCAGG

Clone Rv160

:Rv160SP6.seq:::

ATACTCAAGCTTCGCACGCTCGGCGCGCGGTACCGCCAGGTGCGCCAAACAGATCGTCGATGTTGCGCTCGTCCGC
CTCGCGCACGTGGTCTGTCAACAGTCAACGTTAACGCCGCCGCACATGTCTGCGGCCGGGCAAAAACGTGAAAAACG
AGCGGGCGACTGCNATGTCATGACACCGACGGCCGGATGGGCCAGGGTCTGGCAAATTCGATCTGTGCGGCCAGT
GCCAGCAGCGTCGCCTCGTCATACGGCCGGCCGACGAGTTGAACCGCATGAACGTCGAGAGCAGCCCGCGCAGCAGA
GGCACCACGGGCGCGGGCTGGCCGGTCAGATTCCAAATTGAAAGTACGGAACCGCTGCACCACAA (SEQ ID NO. 121)

:Rv160T7.seq:::

ATCGTTTCGACCAGGCGCTCCATCCGGCGAGTGGATACTCCCAGCAGGTAGCAGGTGCGCCACCACGCTGGTCAGTGCG
CGTTCAGCTCGCTTGGCGCGTGCAGCAGCCAGTCCGGGAAATAGCTGCCCTGGCGCAGCTTGGGGATCGCGACGTGCG
ATGGTTGCGGCACGGGTGTCGAAATCACGGTGGCGGTAGCCGTTGCGCTGATTGGACCGCTCATCGCTGCGTTTCGCGG
TAGCCCGCCCCGCACAGGGCGTCGGCTTCAGCCCCCATCAAGGCGGCGATGAACGTCGAGAGCAGCCCGCGCAGCAGA
TCCGGGCTCGCTGTGCGAGTTGGTCAGCCAGAAGCTGCTCGGTGTCGATAAGATGANAAGAAGTCATTGCGTTATTT
CCT (SEQ ID NO. 122)

Clone Rv161

:Rv161SP6.seq:::

ATACTCAAGCTTGGGTGTTGCCGATCACCGGAAGCCGCATGATCAGCCACGTTTCGCGCCGCCCGGCATACGGCGGGC
TACCGATCTCCGCGTCATACACCCGCGGGTAATCGCCGACGGTGCCGGTTTCGCGAGCCGAAGGTGACGACGCTGATTG
AATCGAGTTCAGGTCCAGCGGGTGGCGCAGCAACGGCGCGAGCTCAACNACGTCAATCACGTTGTGCTTTCTACGG
TCACCGACCCGGTGACCGTAGTCGCGCGGTGCGCTCGGCCGAGAAGTTGCACCGCCACCACCGCGACAACGTCTTGCA
CGCGGACGCCACCCCCCGAT (SEQ ID NO. 123)

:Rv161T7.seq:::

GCGCNAACAGCTCGCGGCAGCCACGACGTGCTGCGTCGGATTGCCGGCGGCGAGATCAATTCCAGGCAGCTCCCGGA
CAATGCGGCTCTGCTGGCCCGCAACGAAGGACTCGAGGTCAACCCCGGTGCCCGGGTCTGGTGCACCTGCCGATCGC
ACAGGTTGGCCCAACAACCGGCCGCTTGATGCCCGGTGCGCAAGCCCGGCAGTTGCCAAACCCAGCGTGATCAGGCTCG
GCTCGCGAGTTCGCGCAAAAAGTGGCTCGCTGATCACCTACCATCGGCCAGGATCTGCGTGTATCACGACGCTCGC
CAAGGAGGTTGTTGTTGCTATCGACGGCCTTTAGCCAGATGTTCCGAATCGACTATCCGATAGTGTCCGCGCCAAT
GGACTTGATCGCCGGCGGTGAGCTGGCTGCCGNGT (SEQ ID NO. 124)

Clone Rv162

:Rv162SP6.seq:::

ATACTCAAGCTTTCTCCGATACCCGCCATGTGCGGCACATCCAGGACTTCTGGGGGATCCGCTGACAGCGGCGGGAT
CCCAAAGTCCGGATGATCGGGCCGCTACGTCGTGGTGTACCTCGTCGGTAACAACGAAACCGAAGCGTATGACTCGG
TCCACGCGGTGCGGCACATGGTGGACACCACACCGCCACCGCAGGGGTGAAGGCCTATGTACCCGTCGCGCAGCAC
TCAATGCCGACAGGCCGAGGCCGAAACAAAGTATCGTAAGGTCAACCGCATCACGAACATGGTGATCGCAGCAA
TGTTGCTAGTGATCTATCGTCCG (SEQ ID NO. 125)

:Rv162T7.seq:::

CCATGAGCACCGCCAGCCGAGCAGAGGCCAACTCCGCCGACGAGGCCGTTGGACTTGTGCTGCTGGACAAGGGG
TTTAGCCGCCGAAGCAGTGACGTACATCGGCGAAGAGCAGTTGCGCTGTCGACCGACGGCGCAAACCGTGAGGCTAGG
GAAGCGAGGAGCACATGGCCGCCGACCCGCAATGTACACGCTGCAAGCAAACCATCGAACCCGGATGGCTATACATCA
CCGCCATCGCCGCGGTCAAGCCGGGATCGTCGATGACGGCGCAGTACTGATTACGTGCCCGGTGAATGCCGCACCC
CGGGGAGCACTTTCCGCCAAAATAACCCGGTTGG (SEQ ID NO. 126)

Clone Rv163

:Rv163SP6.seq:::

CGGGTGTCAATTGGCCACCGGCGGCGGTGTCCGGGAAATGGCGGGTCCCCGGTGGTTTTGCTGAGGAGTGCTGAACCG
TAGTCGAAGTGGGCGGCGTCAGACTCCACCCAGCCAGGAGCGCGGAANCTGAATCCTCCAACCGGGTTGTCNATC
CGGACAGGTTGGGCTGCGTTTGGGGCAATNACAGGTGGCGGCGGTGCGTTCCGGTTCGGCCGGCGGAGGTGCTGCNTTG
GGATCCCCGGTGGGCATTGCGCNTGTTGGCGGCGGCGGTGGTGGGGGGGCAACACGTGTCNCCGGTGGCGGTGGC
CCT (SEQ ID NO. 127)

:Rv163T7.seq:::

CCAAGATCTACACCATCGAATACGACGGCGTCGCCGACTTTCGGCGGTACCCGCTCAACTTTGTGTCGACCCTCAACG
CCATTGCCGGCACCTACTACGTGCACTCCAATACTTCATCCTGACGCCGGAACAANTTGACGCAGCGGTTCCGCTGA

CCAATACGGTCCGTCCCACGATGACCCAGTACTACATCATTCGCACGGAGAACCTGCCGCTGCTAGAGCCACTGCGAT
CGGTGCCGATCGTGGGGANACCCACTGGCGAACCTGGGTTCAACCAAACCTGAAGGTGATTGTAACTGGGCTACGG
CGACCCGGCCTATGGTTATTCGACCTCGCCGCCAAATGTTG (SEQ ID NO. 128)

Clone Rv164

:Rv164SP6.seq::

AGCTTCCCGAGTTCGGCTTTGGATCAAGACCCAGTCCGCGGGCGCGATCCGGCNGCTCGGTGACTACATCAAGCCAC
AAATCGACGGCTTTCCGGGTGCCGATACCGATGACGTGGCGGATGTCGAGTGTTGAGTTCTCGGCGGGGCGGATGCTC
ACCTGGCGATCACCTGCCTCTCGTTGACGATCGATCGTCTATGCCGCCGTCTCTGCGGGAACAGGCCNCCAGTACATC
GCCACAGACGGGATCCACCCGATTTCCGGCTACGTTGCTCGTTTCGGTGTTCCGACTAGTCGGTCTGGTGACGTGC
CGGTGATGCGGACCGGTCCTAGCACTGACCAATGGCCAAATGCGGGC (SEQ ID NO. 129)

:Rv164T7.seq::

CGGGGGGCTCTTAATAGTGTAGGAAAGAGCTCTACATATTCAGGAGGATTCACCATGGCTCGTGCGGTCCGGATCG
ACCTCGGGACCACTCCGTCGTCTCGGTTCTGGAAGGTGGCGACCCGGTCCGTCGCCAACTCCGAGGGCTCCA
GGACACCCGTCATTTGTCGCTTCGCCCGCAACGGTGAGGTGCTGGTCTGCCAGCCCGCCAAGAACCAGGCAGTGA
CCAACGTCGATCGCACCGTGCCTCGGTCAAGCGACATGGGCAGCGACTGGTCCATAGAGATTGACGGCAAGAAAT
ACACCGCGCCGAGATCAGCGCCCGCATTCTGATGAAGCTGAAGCGCGACGCCGAGGCTACCTCGGTGAGGACATTA
CCGACGCGGTTATCAGACGCGCCGCTACTTCAATGACGCGCCAGCGTCAGGCCACCAAGGACCCGGCCAGATCGCCGG
TCTCACGTGCTGCGG (SEQ ID NO. 130)

Clone Rv165

:Rv165SP6.seq::

ATACTCAAGCTTCATAACAGGCCTGTTGTGGGCGCACCCGGCTCGCCGAGTCTGCACGCACCGCCTCAAGTGCGGCC
CGCACCGCCGCGATCTCCCGGTACGCGAGGGCCGCGGCCCGCGCCGCGAGCGACGGCGTTCGCGCGAGTTCGCCGTCA
ATGATGCTGACCTGATCGGCCACCCGGGCGTTCTCGGCGTCTTCGCGTTCACTAATCGCGGTGCTCAGCAGCGTCTCG
ACAGCCACACCCGAGTGGCGACCACTGCTCCACCACGGACCGCAGCGATGCCGTACCTCACCGTCCAGCGGTCC
ACCACGACACGGTCTGTCACCAAGCGCGCGGGCATTCAACCAACCGCGGTACCGCCAGGCCGATCGCCACACCCGCC
ACCATCCCGATGCAGCCAGGCCGGGAGTAAGA (SEQ ID NO. 131)

:Rv165T7.seq::

CTGGTGTGACGGAGCCTAGTACAACCTCCTCTCCAATGCTCTTGCCCCGATCGCGGGCAGCAGGATGACCCAGGAC
ATCCTGCCGCCCGAAGTACTGGAAAAGCTCACACCCGAGTTCTGTCGACCCGGTGGTGGCCTACCTGTGCACCGAGGAG
TGTGCCGACAACCCATCGGTGTACGTCTGAGTGGTGGTTAGGTGCAGCGAGTTGCGCTGTTTGGCAACGACGGCGCC
AACTTCGACAAACCGCCGTCNGTACAAGATGTTGCGGCGCGGTGGGCGGAGATCNCCGATCTGTCCGGTGCGAAAATT
GCTGGATTCAAGTTGTAGAACTAAAT (SEQ ID NO. 132)

Clone Rv166

:Rv166SP6.seq::

ATACTCAAGCTTTTCCGGCGTCTCCACCTGACCCAAAAAGCGCAGGTGCGCCGCCAAACGGCCCGCTGGCCGCGCA
ACTGGTCCGCGTCCGCGTGGCCGACAATCAGTAGCTGGACATCCGGAAACCGCTGCACCACCTTCGGCAGCGCGTCAA
GCAAAACGGCCATTCC (SEQ ID NO. 133)

:Rv166T7.seq::

TTTCAGATCTCATTTTTATGACATGACTGGAGATCTGTCTAGATTGCAGCTCCTGTGAGCGTGGGTACCGGATTCAAG
CCGGTCCGTCACGCCGCGGTGGTACCGGCTTTGCGGCAGTGCTCGGCCCTCGAGTTCCGGCGATCGCGCGCGAAGTGCGT
TTGCGCGACCAAGATCGCGGCCTAATGGCCGGCGATGACCGCGATGACCAGCGCGATCCAGGAAAAACCGTTCCAACC
AGTGCTGGGCGGCCATCCCCG (SEQ ID NO. 134)

Clone Rv167

:Rv167SP6.seq::

ATACTCAAGCTTCCCGACCACAAGTTGAACAGCACCGATTTCCGGCGAGCACTTCGTCAACTTCCAGGGTGCCCGCACC
AAGTATTTGACAAGTATTTCCGTGGGGCCGCCGCCCGCGCGCGCAGGTGGTTCATCCTGGCGCGGGGCTGGAC
TCCCGCGCGTACCGGCTGCCTTGGCCCCAGGGACACGGTTTTTGAGCTGGACCGCCCGCAGGTCCTTGATTTCAG
CGCGAGGTGCTCGCCAGCCACGGTGCCCAACCGCGCGCCCTGCGCCCGCA (SEQ ID NO. 135)

:Rv167T7.seq::

GTGTGCTGTCAATTCAGAGCTGAGCCTGATGCACTCAACTTACTGAGCATGCTAACGCTGGTCTGCGGGTCTGTTC
CCGCGTGTCCGACGGGCACACGCTCGGGCGTAGCTGGGAGAGGCCCGGTCAAGCCCGAGAGCAGTGCTCAGTCCG

CCAGCTTGACCGACTTTTCGATGAGAACGCGCTTCTCGCCGTATTGAACTGGCGTGCTGACGGTCGCTGAGCAGCGCTC
GCCGAGTGCGGCCGCTGATTCTTTTCATCGAGCCAGGAGGCGCATTCGTGTTTCGGCCGCCTGCGGGTCGGCCCCATCGT
CGACGCGATCCGTCACCCACTCCTCGATCAGGTCTGCCTCATCGAACGGGCCAACGGTGCTGTCGGAGTATGTGTGCG
TGGGCACGGCGAGCCGGGTGCTGTGGTACACCACCGTTGCATGACCAAGTTGACGCCCTGACTGGCTGAGCACCAGCGA
TCCGCTCACAGGTCGGAACGTTGGTG (SEQ ID NO. 136)

Clone Rv169

.....Rv169SP6.seq:.....
ATACTCAAGCTTTTGGTCTAGCCGGCCGAGCCCGATACAGGTGTATTGGCCACCGCGCGGGCTGTCCGGGAAATGG
CGGGTCCCCGGTGGTTTGTGAGGAGTGCTGAACCGTATGCGAAGTGGGCGGCGTCAGACTCCACCCAGCCAGCAGG
CAGCGCGAAACTGAATCCTCAACCGGGTTGTGATCCGGACAGGTTGGGGTGCCTTTGGGGCAATGACAGGTGGCGG
CGGTGCGTCCGGGTGCGCCGGCGGGAAGTGCTGCGTTGGGATCGCCCGGCTGGGCATTCTGCGTGTGGCGCGGCGCGG
TGGTGGGGGGGCAACAGGTGTCTCCGGTGCGGGTGGCGCTGCACC (SEQ ID NO. 137)

.....Rv169T7.seq:.....
GGGGCCACTCCGCACAATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTCGCCGACTTTCCGCGGTAC
CCGCTCAACTTTGTGTCGACCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAATACTTCACTGACGCCG
GAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGACCCAGTACTACATCATTCGCACGGAG
AACCTGCCGTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGGTTCAACCAAATTG
AAGGTGATTGTTAACCTGGGCTACGGCGACCCGGCTATGGTTATTGACCTCGCCGCCCAATGTTGCGACTCCGTTT
GGGTGTTCCAGAGGTGACCCCGGTGCTCATCGCCGACGCTCTCGTCGCCGGGACCCAGCACGGAAT (SEQ ID NO. 138)

Clone Rv16

.....Rv16SP6.seq:.....
TTCTNTCTTCCNNATTCTGNNNTCTCNTACTACCNNGGCCNCAAAACACCTTGGCNAACGCTCAAAGGCGNTACNGG
CACCAAGGCCCCACACGTACCCCTGTGACCTCCTGCGCCGACCCCGCCGAGGTCTGGCCGTTACCACTGAACGGGC
GAGCCGGGAGTCTGGTACGCATCGAACAAGAGCAAGGTGCATGGGCGGAGTTGTTCCGCCNCTTTTTTATGACGGG
GTGATCCATTGAGGTCCGTGCGCGCGTCGGTCGAGTGGCGGTCACTCCAGGTACTCGACCTCNAGACGAGAGG
ACTCGATCCCATCTANGTGTGGACNAAACAGATCTTCTGTCCGACGACTACACACCACCCAGGCCATCGCCGCCGCC
GCGATGCCAACTTNCACNCCGTNCTGGCCCCGGCGGCGGCGCTCCCCGTTGTCAAACACCTGCCGTGTTCTGTTACN
CACTGCCCAACATCNAGCCCGANCNATCCNAGGTCCGTCCAACGCCCTCCGCGGCTCNCCAACTNCTCCNCTGATCN
TCCGCACCAAAACATGCCGACTCCNTGCNCCNATTGCTTGNATCCCT (SEQ ID NO. 139)

.....Rv16T7.seq:.....
CCGCTATCGGTGCGTGTGCTTGGCGGCGTCGGTATCAACACCGCCACGAAATGGGGCACAAGAAGGATTGCTGGAG
CGGTGGCTGTCAAGATCACCTCGCCAGACCTGCTACGGGCACTTCTACATCGAGCACAACCGTGGCCATCACGTC
CGGGTGTCCACACCGGAGGACCCGGCGTCGGCGCGGTTCCGGCAGACGTTGTGGGAGTTCTGCCCCGAGTGTATC
GGCGGCTTGCCTCGGCCGTTTATTGGAGGCCCCAACGGTCGCTCGGCTCGGCGTCAGCCCCCTGGAATCCCATGACG
TATCTGCGCAACGACGTGCTCAACGCGTGGCTGATGTGCGTGGTGTGTTGGGGTGGGCTGATCGCGGTCTTCGGCCCC
GCGCTGATCCCGTTCGTATCATCCAGGCAGTCTTCGGCTTCAG (SEQ ID NO. 140)

Clone Rv170

.....Rv170SP6.seq:.....
ATACTCATGCTTGCCGAAGTTCGGATGGGTGCGCGCGGCGANCCAGCGAAGTCGCTAGCGTGGCCGTGTTCTTGGCT
TCGGATCTATCCTCGTACATGACCGGCACCGTGTGGACGTGACTGGCGGCCGTTTCATATGACACCGAGATCATTGC
CACGGTACGGCAATTCTGTCAAGAAGGAAATCTTTCCCAATGCACCGGCCCTCGAACGTGGCAACAGTACCCGCAAGA
AATCGTCGATCGGCTGGGTGTTATTGGCTTGTGCGTTCGCCGCTGCAAGGGTATCGACACCACCGAGTTCATTCTCC
GGCGTGCC (SEQ ID NO. 141)

.....Rv170T7.seq:.....
GGCGTCAACGGTGTGCGCACCGGCGTCTGCAAGTGGTAGGCTGCAAGTTGTGATCAGGCCGATGCCGCGGCCCTC
GTGGCCACGATGTACAGCACCACGCCGCGCCCTCACGGGCGACCATCGCCAGCGCGGCGTCCAGCTGAGGCCCGCA
ATCGCAGCGGCGTGACCCAAACACATCGCCGGTCAAGCACTCCGAATGCACCGGACAGCAGTCTGACCGTCCGCG
GTTGGGCCGCGGATCTCGCCGCGGACAGCGGACATGTTCCACGTCTCTAGATGCTGGTGTAGCCGATGGCGCG
AATCTCCATGACGAGTCGGAATCCGCGCCTCGCG (SEQ ID NO. 142)

Clone Rv171

.....Rv171SP6.seq:.....
ATACTCAAGCTTCGGCCTCGCTGCAGGAGTGGGAGCCGCAGGGCTGGAAATCCGAAAAACGAGCCGGTGATCGCACTG
TCGCCGATCGGGGCCGACCTGGTTGGTGTACCGATGAATCCGCACCCAAAATGTGGCTGCGGTGGCGTTTCTTGAC
TCCTTGGCGTCGACTCTTGTGGCAGCCACCGAGCGGTTGGTCCAGGATCTGGATGGGCAAAGTTGTGCGGCCCGGCCG
GTGACGGCCGATGAGCTGACCGAGGTCGACAGCGCCGTGTGGCTGACTTGAACCGACATGGATTGCCCCGGTTGG
CGTCACCTCAAGCATTTCAATGGTTAT (SEQ ID NO. 143)

.....Rv171T7.seq:.....
ATGCGTCACCCGATGCGCCAGATCGGGGCTTCGCAATAAAGCACGAACAGGCGGGCAAACGTCTATCTCGGAGC
CGGAAGGGCAATCAGCCGACCGTCGACGAACGACACCGGCGATAACCACTTAGGCGTTGAACGGCCGGCCCAAACATT
ACGCTCCGTTGATAAGGCTTTCGGTCTCTTCCCGGTCATCCCAAGCACCTTGCGGCAAATTTGAACGCTTTCCTGT
CCGGGCACCGCCCCGGGCTTTGGGGTCCNTCCGA (SEQ ID NO. 144)

Clone Rv172

.....Rv172SP6.seq:.....
ATACTCAAGCTTCAATCGCGCCGCCACAATCCAAATATGCGTCTAGCGTCTCGATGAGCGTCGGTCCGGCATCGGCTA
GGGGCCGCATCACGTGCGTATGAGGGCCACGATCGCCCAAGGCGTCGCCCATCAAGGGCGCGTTCGGGCAAATTC
CCCTATCCAGCACGGGCCGCGCGCTCCGCNCCAGCCGGCGACGGCGTTCATCCCGGAGATCGCCTCGCTAGCGCTGC
GGTGCGCCGCGGTGAGCATGGGCGCCGTGGGGCCGATGACCACCGGGGCGT (SEQ ID NO. 145)

.....Rv172T7.seq:.....
TTCGGCGGGTCTGTAGATTGCGGTGCGCCACCCACAGGCACTCATGAACCGCAGCCACGATCGATCTCGGTGG
(SEQ ID NO. 146)

Clone Rv173

.....Rv173SP6.seq:.....
GCGCACCATCGCCAGTAGGTGCCCCTGGTGGGCGCGTCGAGCCACCCGAGCGGAAACGCGAGTCCGAACAGCAACAG
CAGGACGGGCGCAACCAGGGCGGTGACCATGCCCCCGGCGCTGAACATCAACCACGGAAGGGCTCCGCCGAGCGTCC
GCGCGACC (SEQ ID NO. 147)

.....Rv173T7.seq:.....
CATCGTCGAACCTCGGTCCGGTTGNTAGNACCGCAGCACCAAACGCACCCACCGACCCCCACGCTTCACGCCAACCC
TTTAGTTTCATTGGCGTGAACAGCAGCGTAGCCGTTGCCCGATATATGTGGAAAAATCGTTCGGACGTACAAAAAAA
GTTCTGACGCTGGCGTCAACTCGAAATGCCTCGGAAGTCAATGATGATCCATCAGTCAATATTAAAGTCG
(SEQ ID NO. 148)

Clone Rv174

.....Rv174SP6.seq:.....
ATACTCAAGCTTGTCTGCTGCCTCAGCGTATGCATCCAACAGCGCATCGCGATCAACGATCAGGCGCGCCGATTTGGG
GCCGCGGGCAGTGGCACTGGCCAGATGGCCGTTTTTTTCGAGAACTTCAACGCTGAGCGCTGCTTCCCATCGAGAG
ACCGGTGGCCTCTACAACCGATGCGACAGTTGGACCGGCGATGTTCCGACGACGCGTTACATACGGCAAGTNTGGC
GCGG (SEQ ID NO. 149)

.....Rv174T7.seq:.....
TTGTCCAGGCGGGGAATCGGGCAGGGAGACGACACCTTCGTTGCGTTCGATCGTCGGAACGGGTAGTTGGCCGCGAC
CACGTTGTTTCGGGTGAGCGGTTGAAAAGTGTGACTTGCCGACGTTGGGCAGGCCACGATCCCCAGGCTCAAGCT
CACAGA (SEQ ID NO. 150)

Clone Rv175

.....Rv175SP6.seq:.....
ATACTCATGCTTGGCGCCTGGGTGGCAGCCACCTGCCACCACACGGACCGCGGTGCGGACGCGGCTGACCGGCCTG
GTGGTCAGCATCGTGGCCGGTCTGCTGTTGTATGCCAACTTCCCGCCGCAACTGCTGGTGGGCGGGCGGTGGTTGCC
CTCGCATGCTGGCCTGGGTGCTGACCCNCCGCNCAACACCGGTGGGTGGGCTGGGCTACGGCCTGCTATTCCGC
CTGGTGTCTACGTCTCGTTGTTGCCGTGGATCGGCGAGCTGGTGGGCCCCGGGCCCTGGTTGGCACTGGCGACGACG
TNCGCGCTGTTCCCCGGCATCTTCGGTCTGTTCCGCGTCTGTTGACCTGTTGCCGGTTGGCCC (SEQ ID NO. 151)

.....Rv175T7.seq:.....
CGCCAATTACGATATCGTTAACCGATATCCCGAGCCGATAGCTGGCGGGCTCGGGTGGTGGCCAGCGGCGCTGCGAC
GAAAGGTGTGACCGTCATGAAACAGACACCACCGGCGGCGTGGCCGTCGTCACCTGCTCAGATCTCAGCATCCGC

AGCCGGTGTGATCGCGCTTTCGGCGTGTAGTGGGTCGCCGCCGACCCCGGCAAAGGCCGGCCCGACACAACCCCGGA
ACAGGAAGTCCCGGTACCGCGCCCGAAGNACTTGATGCGCGAACNCGGAGTGCTCCAAACGCATCCTGCTGAT

(SEQ ID NO. 152)

Clone Rv176

.....Rv176SP6.seq:.....

ATACTCAAGCTTGGGCACTGACTTCGGTACCCCTCCGCCTTTGGCCAGCAGCAGCCACAGCGCGGTTGCGGGACCGA
ACGTGGACATCAATAGCCCGGAATCGGTGTGTGCAAGTTGGTAAACGGTGTGATCCCAAGCTTTGCCAGCCTTTTCG
TAGTCTTGGGCCCCACACCCACAGTGCTTCGACGGTACGGTACCCATGATGGCCATCCAGTTGGCATCGGTGAGCT
GATAAATGCCAGCTGGTTTCGCCAACCCGGTAGCGATCTTGGCGCGCTGCTTGTGCTCACTGATACCTATCGAGCAAG
ACAGCCCGGTTTGGCAGAAAATGACTTTTCGGATCTCTTCGGCGACTTCGATGGGGTCGTGGGA (SEQ ID NO. 153)

.....Rv176T7.seq:.....

AAAGTCCTGTGCCGGTTCGCTAAACACCCGGCGGACACTCAGACGGTGCTGGTGGTGCGGCATGGCACCAGCGGGCAGC
AAAGCGCACTTCTCCGGGGACGACAGCAAGCGACCGCTAGACAAGAGGGGTGCTGCGCAGGCAGAAACGTTGGTACA
CAGCTGCTGGCGTTTCGGCGCCACCGATGTTTATGCCGCCGACCGGGTGCGCTGCCACCAGACGATGGAGCCACTCGCC
GCGGAAGTGAACGTGACCATAACA (SEQ ID NO. 154)

Clone Rv177

.....Rv177SP6.seq:.....

ATACTCAAGCTTGGGTTCACGCCCCGCGCAGCCACGCCGTACCTTTCCACGAGACCTCACCTGCCGATCCGAAATGG
AATCGGCCGTGACGGAATTGGCGCACCAGAACACCCAACGAGGTGGTGGCTTCGTGCGCAACCGTCACCCGAGTCGCGG
CCACCGTGCGCAGGCGACGTTCTACACCCGACCAAGATCCGAAAGCTGCAAGCTCCAGCACCAGTCCCGACGTCA
TCACCGCTGCCGCCCGGCACGTCTTGACCTATTCGAGCTGGATCGGCCCGTCCGGTTGCTGGGAGTGCGGTTAGAAC
TGGCCTAGAACCGCGGGGCACACCGCNCCTGGGCGGGGCGAATTCTTGACCGCNCCTGGCC (SEQ ID NO. 155)

.....Rv177T7.seq:.....

CGCGGTTGGCGTAGTTGGACGGGTCGCCCTCCGAGGCCAATGATGACGATGACCACGCCGATCACGATGGCCACCAG
AGGGACAACAACAGAAAGCTGACGAATCCCTCCTTGGCGGCCGGGGCTTTGTGGTCCCGGTCCGATGGGCGCGAAT
TTACGGCCCCGTCCCCAGGCCGCCGCGAAGCAGGGTCCCCAGCCAGTTGGCGTAGGCGGAATTAACGATCAGCGCCA
CCGCGATAACCTGCCATGCCTCGGGCATATCGATGTGCGGCCAGAACAGGCCGAAC (SEQ ID NO. 156)

Clone Rv178

.....Rv178SP6.seq:.....

CCAACAAGAGCATCGGGACATACGGAGTCAACTACCCGGCCAACGGTGATTTCTTGGCCGCCGCTGACGGCGCGAACG
ACGCCAGCGACCACATTACAGCAGATGGCCAGCGCGTGCCGGGCCACGAGGTTGGTGCTCGGCGGCTACTCCAGGGTG
CGGCGGTGATCGACATCGTCACCGCCGCAACCACTGCCCGGCTCGGGTTACGCAGCCGTTGCCGCCCGCAGCGGACG
ATCAGATCGCCGCGATCGCCCTGTTGCGGAATCCCTCGGGCCGCGCTGGCGGGCTGATGAGCGCCCTGACCCCTCAAT
TCGGGTCCAAGACATCANCTCTGCAACAACGGCGACCCGATTGTTTCNACGGCAACCGGTGGCGAGCGCACCTAG
GCTACGTGCCGGGATGACCAACCAGGCGGCGGTTTCGTGCGGAGCAGGATCTAACCGCGAGCCGCCCATAGATTCC
CG (SEQ ID NO. 157)

.....Rv178T7.seq:.....

TAANACCCGTGTAATTTGGGATGGGCAAAAAGGCCAAGCACCGCGTGCCACGAACGCCGGGAGGGACAATCTCGGGC
GGTAGGGCTTCTCGCGGGAAGGCCCGAACGTACGGCGTTTCAACACGTGCGCTCNCCTCCGACCGCGAACATTTCG
GGATGGCAGCAACCTGGTAGCNCCTGGCCGGGCGATGATCTGCAGCGTCGCCCGGGTAGTCGCCGCCCGGGCGGCT
ACAGTCTGAAACGCGATGACCATCGATGTGTGGATGCAGCATCCGACGCAACGGTTCCTACACGGCGATATGTTCCGC
TCGCTGCGCGGTGGACCGGTGGTCTATCCCGGAGACCGACNTCCGATCGAAGCGACCGTCTCCTCGATGGACGCC
GGCGGCGTCACCTGGGTTTGTCTACCGCCTGGCGTGCCCCAA (SEQ ID NO. 158)

Clone Rv179

.....Rv179SP6.seq:.....

GTCCGCAAAAGACTCAGCGGCCGACTTTGCTCGCAGCTGGCGGTACCGCGCCACCGATTTCGATGCCGTGGTTCGCGGAA
GAATGCCTCCCGAAATCGCACGGCCGACTCCAGTTTCGGCGAGCATCCGCGATGCCAGCTGCGGCTGCGCCCTGCCGGC
CACGGCACCCACATGCGGCAGTTTCGTCCACCTGGGCCAGCGCCCCGCCCGCAAGTCCAAACAATAGAACTGCACCCG
GCCCCATCGTGGGTAGCAGCCAACGCCATGATCAGCGTCCGCGAGCGCGGTTGACTTGCCCGTTTGGGGTGACCTAC
GACCGCGACATTGCCTGCGGCCCGGACAAGTCGATCGTCAGCGGCACCN (SEQ ID NO. 159)

.....Rv179T7.seq:.....
CGTGGCCACGAACGCCGGGAGGGACANTCTCGGGCGGCTAGGGCTTCTCGCGGGAAGGCCCGAACGTACGGCGTTTCA
ACACGTGCGCTGCGCCTCCGACCGCGAACATTCCGGGGATGGCAGCAACCTGGCAGCTACCTGGCCGGGCGATGATCTG
CAGCGTCGCGCGGGTAGTCGCCGCCGGGCGGTACAGTCTGAAACGCGATGACCATCGATGTGTGGATGCATCATC
CGACGCAACGGTTCTACACGGCGATATGTTNCCTCGCTGCGCCGGTGGACCGGTGGGTCTATCCC (SEQ ID NO. 160)

Clone Rv17

.....Rv17SP6.seq:.....
ATACTCAAGCTTTGCGCGGGCGCCGAAATGTGAACGCACCAAACCCGCCCGCTGCGGGTTCGGCGGGCCACTCGACCT
CGAATTTGCGCGCGGTGACCATCCAGCCCGACGGCAGTTGGGCACCCGCCCGCGGTGCGCGGCATAACTGTTGGCGT
CGCCGTATATAAGCTCGAACAGCACCGAAACCGACTCCACCACCGGCCGGTGCGCCTCAAAATCCACGCCGATCTCCA
CATACCGGGAACGTCGGTGTCCCATCGGGTTTCGGCTTGGCCGCCAGCTGCACACCACCGGTGGCCTCGGCCACCT
TCGCGGCCTGAGCGCAGCTACNCATCCTGACGATCATCACCCGCCCGCGGTACAGCTTGGCCTCCGTGACCGCACC
CATCGCCCGGTTGCGCGCACCGCGACGCCGTACAGCCGCGCGCAC (SEQ ID NO. 161)

.....Rv17T7.seq:.....
AGCTTGCCGGGACTGCGGAACAGAAGCGGCGGTTCTACCGCGGTGTGCGGCCGGCGCGATATCGGCCTTTTTACTAA
CCGAACCCGATGTGGGCTCCGATCCGGCGCGCATGGCATCGACGGCGACGCCGATCGATGACGGCCAGGCTTACGAGC
TTGAGGGTGTGAAGTTGTGGACCACCAACGGTGTGGTAGCGACCTGCTAGTGGTTATGGCGGGGTACCGCGCAGTG
AAGGCGACCGAGGGGAATCAGCGCCTTTGTCTGTCGAGGCTGATTGCGCCGGGATCACCCTGGAGCGGGCAACAAGT
TCATGGGACTGCGTGGCATCNAAAACGGCGTGACCCGGCTTCATCGCGTCNGGGTGGCCAAAGACAACCTTGATCGGCA
(SEQ ID NO. 162)

Clone Rv180

.....Rv180SP6.seq:.....
CTCAAGCTTGCGGATGCGGGCTGGCCAAAACCTGGCCGGGCGGGGGTTGGCTTGTTCATCAAGGGTGGGTGCGG
(SEQ ID NO. 163)
.....Rv180T7.seq:.....
CCGAAGGCCCGTTCCCGGGCGTTCAGCAAGCGATCGTCGGTTGGCCCACTGCGGGTCAATCTTGCGGCCGCGCCGGT
CGTGAACGCCCAGGTCACCCGGCGGCGTACC (SEQ ID NO. 164)

Clone Rv181

.....Rv181SP6.seq:.....
ATACTCAAGCTTTTTTCTGCTCATGAAGGTTAGATGCCTGCTGCTTAAGTAATTCCTCTTTATCTGTAAAGCTTTTT
GAAGTGCATCACCTGACCGGGCAAATAGTTCACCGGGGTGAGAAAAAGAGCAACAACCTGATTTAGGCAATTTGGCGG
TGTTGATACAGCGGGTAATAATCTTACGTGAAATATTTCCGCATCAGCCAGCGCAGAAATATTTCCAGCAAATTCAT
TCTGCAATCGGCTTGATACACGCTGACCACGTTTATAAGCACTTGTGCGGCGATAATCGTTACCCAATCTGGATAATG
CAGCCATCTGCTCATCATCCAGCTCGCCAACAGAACACGATAATCACTTTCGGTAAGTGCAGCAGCTTACGACGGC
GACTCCCATCGGCAATTTCTATGACACCAGATACTCTTCGACCGAACGCCGGTGTCTGTTGACCA (SEQ ID NO. 165)

Clone Rv182

.....Rv182SP6.seq:.....
CTCAAGCTTGGTGCCGACATGGCCGGGCTGGAGCCCGCGTATGGCAAGGTTCCGCTCAATGTGGTTGTGATGCAGCAG
GACTACGTTTCGCTCAATCAGCTCAAACGTCACCCCGTGGCGTGCTGCGCAGCATGAAGGTCGGCGCCCGCACCAGT
TGGGCGAAGGCAACAGGTAACACCTGGTCGGCATGGGTGAGCCCTCATTGGGCGGTTGCGGATCGGGTTGCACCGC
GCCGGAGTGCCGGTCAACTCAACACCGCCTTCACCGATCTTTTCGTCAAAAATGGCGTCTGTCGGGGTATAC
(SEQ ID NO. 166)

.....Rv182T7.seq:.....
CCGAAGCGTGGGAAATCCTGACCGAATACCGCGACGTGCTGGACACTTTGGCCGGCGAGCTGCTGGAAAAGGAGACCC
TGACCGACCCGAGCTGGAAAGCATCTTCGCTGACGTCTAAAGCGGCCCGGGCTCACCATGTTTCGACGACTTCCGGTG
GCCGGATCCCGTCGGACAAACCGCCCATCAAGACACCGGGGAGATCGCGATCGAAACGCGCGGAACTTGGGCC
(SEQ ID NO. 167)

.....Rv183SP6.seq:.....
CGACTCGACAAGCATTCTTGACAGTTGTTTTGGCTCGGCATGGTTAGCCAAGGTTCTGCGGTCCCACCAGATCATCTT
GGTCCGGTAGCGCTCGTCCGGGTATGCTGCCGCCGGGATTCTCGCTGCTATTACTCCCCGAAAAACGCCACCGGTC
CAGCGCTGGGCGCGCGGTCCCATCACAACTGAACCCCCAACAGGGGACATGCTTAGCGGTAGGGCGCGCGCCA
AGGCGGCAGCAATCGCATCACTGCGCTGCGCGTCACTATTAAACCCACCGGACTTCACTTCCACGACCCCGAATGGCG
CCCGGTCAATTGATCATCTTGCACACCGCGGATAATCCGGGATTGCCAGCCCATTCGACTACCGCATGGGAGTCATCGG
CTGACCGCAGCGGTCCGATTACCGGAGCGCCCCGANTACATCTCTCCAATATCAATGGGCGCAA (SEQ ID NO. 168)

Clone Rv183

.....Rv183T7.seq:.....
GCGGTNTAGCTTCCCGTCGTACCGGCGACCGCCAGCCGAGAAGCTCGTTTTCCAGTGTTGCTGGGGATTCTCACGCT
GCTGCTGAGTGCCTGCCAGACCGCTTCCGCTTCGGGTTACAACGAGCCGCGGGGTACGATCGTGCGACGCTGAAGTT
GGTGTCTCCATGGACTTGGGGATGTGCCTGAACCGGTTACCTACGACTCCAAGCTGGCGCCGTCTCGTCCGCAGGT
CGTTGCTTGCATAGCCGGGAGGCCCGGATCCGCAATGACGGATTCCATGCCAACGCTCCGAGTTGCATGCGGATCGA
CTACGAATTGATACCCAGAACCATCGGGCGTATTACTGCCTGAAGTACCTGGTGGGGTCGGATACTGCTATCCGGC
GGTGACGACCCCGGCAAGCCGCCATCCGTGCTGCTGT (SEQ ID NO. 169)

Clone Rv184

.....Rv184SP6.seq:.....
CTCAAGCTTGGGCGTGACGGCCACCGGGCCACTCCGCACAATCTGTACCCGACCAAGATCTACACCATCGAATACGA
CGGCGTCGCCGACTTTCCGCGGTACCCGCTCAACTTTGTGTGCGACCTCAACGCCATTGCCGGCACCTACTACGTGCA
CTCCAATACTTTCATCCTGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGAC
CCAGTACTACATCATTGCGACGGAGAACCTGCCGCTGCTAAAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACT
GGCGAACCTGGTTCAACCAACTTGAAGGTGATTGTTAACCTGGGCTACGGCGACCCGGCCTATGGTTATTCC
(SEQ ID NO. 170)

.....Rv184T7.seq:.....
CGGGTGTCTATTGGCCACCGGCGCGGCTGTCCGGGAAATGGCGGGTCCCCGGTGGTTTTGCTGAGGAGTGCTGAACCG
TAGTCGAAGTGGGCGGCGTCAGACTCCACCCAGCGAGGAGCGCGAAGCTGAATCCTCCAACCGGGTTGTCGATC
CGGACAGGTTGGGGTGCCTTTGGGGCAATGACAGGTGGCGGCGGTGCGTTCGGGTGCGCCGGCGGAGGTGCTGCGTTG
GGATCGCCCGGCTGGGCATTGCGGCTGTTGGCGGCGGCCGGTGGTGGGGGGCAACANGTGTGCGCGGTGCGGGTGCG
GCTGCA (SEQ ID NO. 171)

Clone Rv185

.....Rv185SP6.seq:.....
NCTTGATATTGGCGTCAACGGTGTGCGCACCGGCTCCTGCAGTTGGTAGGCCTGCAGTTTGTGCATCAGGCCGATGC
CGCGGCCCTCGTGGCCACGATGTACAGCACCGCCGCGCCCTCACGGGCGACCATCGCCAGCGCGGCGTCCAGCT
GAGGCCCGCAATCGCAGCGGCGTGACCCAAACACATCGCCGGTCAAGCACTCCGAATGCACCCGGACGACGTCGT
CACCGTCGGCGTTGGGCCCCGGCGATCTCGCCGCGGACCAGCGCGACATGTTCCACGTCCTCGTAGATGCTGGTGTAGC
CGATGGCGCGAAACTCCCATGACGAGTCGGAATCCGCGCCTCGGCGACCCGCTCAATGTGCTTCTCGTGCTTGCGCC
GCCATTGATCAAGTCAGCAATGGTGATCAGCGCCAGACCGTGCTCNTCGGCG (SEQ ID NO. 172)

.....Rv185T7.seq:.....
CATAAGGGCCGGCGTACCCGGTACCGGCCGCGGGCTACACGTCGCCGGAATGGAAGCGCAGTAAGCCCTCAACGCG
CCACCGCTTTGGCCCCGCGCGCCCGGCTAGGCGCATCGGCGGTGGCCGTGGGCGGGCGCACTGCGACCTCACCAGCGG
CTTTCGAGCTTTGTTGATCAACCGGCCAGCATGGTCGAGGATGCATTGAGACCATATTGAAATTGGTTTCATCGG
GGGCCCCGATCGGATGCCCTCCAGTTGCGTGAGCAAGCAGCGGAGTCGTGCGGGATCGATGGCCACGGGGTGT
CAATGGCGGATGGTCCGCTGCCCGCCGACTGGCTCTTGCGGGAGAGCCGATCTAGCACCCAGATCCGCGCACGTGGA
CCGAAACCGCCAGTAGATGTGAAAGCGT (SEQ ID NO. 173)

Clone Rv186

.....Rv186SP6.seq:.....
CGTCCTTTTCCCCAAGATAGAAAGGCAGGAGAGTGCTTCTGCATGAATATGAAGATCTGGTACCCATCCGTGATACA
TTGAGGCTGTTCCCTGGGGTCTGTACCTTCCACNAGCAAAACACGTAGCCCTTCAGAGCCNNATCCTGAGCAANAT
GAACAGAAACTGAGGTTTGTAAACGCCACCTTTATGGGCAGCAACCCGATCACCGGTGGAAATAGCTCTTCAGCAC
GTCGCAATCGCGTACCAAACACATCACGCATATGATTAATTTGTTCAATTGTATAACCAACACGTTGCTCAACCCGTC
CTCGAATTTCCATATCCGGGTGCG (SEQ ID NO. 174)

Clone Rv187

.....Rv187SP6.seq:.....
CTCAAGCTTCATGTCCGTACGGCTCGGGTACGCTTCCGTCGAGTGTCGAGTGATAAATGACGACCGGGACCTCGTC
GGCATCTTCCATAGCCCGCCACACCTTCAGTTGCTCACCGGAATCCAACCGGTAGAAGTTCGGCGAGCGCTCGGCATT
GGTCATCGGGATATGCCGCTCGGGACGGTCAGAGCCCTCGGGTCCGGCCAGCACTCCGACGGCTTCGTGCGGGTGGTC
GCGACACGCATGGGCCACCATCGCATTAC (SEQ ID NO. 175)

.....Rv187T7.seq:.....
NCGCCGCCAGCCACCACGCGCGGGTCGGGCGCCGGGCCCCGGGCCAGGCTGCTCCGCTCGGTGATGGCAGGCCACC
GCGACACCACCCGGCTGCGCTACGTCGAGCCATACCGGGCGGAGCTACATCGGCTCGGCCGCCAGTGTTCGGGCCCT
CTTTCGAGGTCGAGGTCGATACCGATTGCGCATCCGCGAGCCGACCCCTGGACGACAGAACCCTGCCCTACGANTGCT
TGTCGGGCGGGGCCAAAGAACAGCTTGGCATCCTGGCGCGATTGGCCGGCGCGGCGCTGGTCTCCAAAGAAGACGCC
TTCCGGTGCTGAT (SEQ ID NO. 176)

Clone Rv188

.....Rv188SP6.seq:.....
CGCCACGTTTCATGGGCAACAACCCGATCACCGGTGGAAATACGCTTTCAGCACGTCGCAATCGCGTACCAAACACAT
CACGCATATGATTAATTTCGTCCAATTGTATAACCAACACGTTGCTCAACCCGTCCTCGAATTTCCATATCCGGGTGCG
GTAGTCGCCCTGCTTTCTCGGCATCTCTGATAGCCTGAGAAGAAACCCCACTAAATCCGCTGCTTCNCCTATTCTCC
AGCGCCGGG (SEQ ID NO. 177)

Clone Rv189

.....Rv189SP6.seq:.....
ATACTCAAGCTTCAACCGATTGACGCATTGTGCGAACTGACGGCGCCCGCGCATGGCCAATCCGGAAGACCATCATTG
GCCAGTGGCCGGGCGCTAACAGGTTCCAGCCCCCACCAGTGCCGCTCGAACATGCGGTGCAACCCATTTCGAGGGCCG
GCAGGGAAAGCACCCGGAAGCCGCAAGGGCTGCAGTTCCGCGCCCAATAGTGTCTCGCAACCCAGATGCGCTCGA
AAACCGCGCCGCGCAGTCAGCGCACCCGACGCGAGGTGGAAGAGACGTCGTCAGCGCGCCACATGGGGTGCCAATCGGC
ACGGCAGGTAGGCCGCGCGCAACCCGAACGCGTGGTGCATGCCACGGTCCGCGAGGAGGCGCAGCACCCGCCAATGCC
GAAGCCACGAAACATCGGGCGCATCCACGCTTCAACCTC (SEQ ID NO. 178)

Clone Rv18

.....Rv18T7.seq:.....
AGCTTTTGGCAGGGTCTCCTTCGAATTCGGCGTGCACCGCTATGGGTTGCAGCAGCGGCTGGCGCCGCACACCCCACT
GGCCCGGGTGTTCGCCCCGAACCCGGATCATGGTGAGCGAAAAGGAGATTGCGCTGTTTCGATGCTGGGATTTCGCCA
CCGCGAGGCCATCGACCGATTACTCGCCACCGGGGTGCGAGAGGTGCCGCGAGTCCCGCTCCGTCGACGTCTCCGACGA
TCCATCCGGCTTCCGCCGTCGGGTGGCGGTAGCCGTCGATGAAATCGCTGCCGGCCGCTACCACAAGGTGATTCTGTC
CCGTTGTGTCGAAGTGCCTTTCGCGATCGACTTTCGTTGACCTACCGGCTGGGGCGTCGGCACAACACCCCGGTGAG
GTCGTTTTTGTGTCAGTTGGGCGGAATCCGTGCTCTGGGTTACAGCCGAATCGTCAC (SEQ ID NO. 179)

Clone Rv190

.....Rv190SP6.seq:.....
ATACTCAAGCTTTGTACACCAACTGTTTCCACAGGCGCTCCATCCGGCGAGTGGATACTCCAGCAGGTAGCAGGT
CGCCACCACGCTGGTCACTGCGCGTTCACTCGCTTGGCGCGCTGCAGCAGCCAGTCCGGGAAATAGCTGCCCTGGCG
CAGCTTGGGGATCGCGACTTCTATGTTGCGGCACGGGTGTGCAATACCGTGGCGGTAGCCGTTGCGCTGATTGGA
CCGCTCATCGCTGCGTTTCGCGGTAGCCCGCCCGCACAGGGCGTCGGCTTCAAGGCGCGGATGAACGTCG
CGAGAGCAGCCCGCGCAGCAGATCCGGGTCGCTGTGCGAGTTGGTCAGCCAGAACCTGCTCGGTGT (SEQ ID NO. 180)

.....Rv190T7.seq:.....
CCTTAAGCCCCGAGGGCCCGGCACGCGCGGTACCGCCAGGTGCGCCAACAGATCGTCGATGTTCCGCTCGTCCGCC
TCGCGCACGTGGTCTGTACCAAGTCAACGTTAACCGCGCCGCACATGTCCTGCGGCCGGGCAAAAACGTGAAAAACGA
GCGGGCGACTGCAATGTCATGACACCGACGGCCCGCGATGGGCCAGGGTCTGGCAGATTTCGATCTGTGCGGCCAGTG
CCAGCAGCGTCGCTCGTCATACGGCCGGCCGACGAGTTGAACCGACATGGGCAGGCCGTCGCCGTCGAAGTCCACG
GCACCACGGCCGCGGGCTGGCCGGTCAGATTCCAGACTTGAAGTACGGAACCCGCTGCACCACCAGCAGCAACGTCG
AAACTGCACCCCGCGGTTGGTAGGCGCCGATGCGGGACGGGCGGTCGCGGCGCCTGGCGTCACAACTACGTCGACAT
CGTCGAAGATCGACTGGATCGGCTGCTCACACCACTCGGCGGCCGAGGCCGCCATCCGCGTC (SEQ ID NO. 181)

Clone Rv191

.....Rv191SP6.seq:.....
AGCTTTTTCGCGTTCGCGCGGGGCGAGCTTCGCGGCAATTCTACTAGCGAGAAGTCTGGCCCGATACGGATCTGACCG
AAGTCGCTGCGGTGCAGCCACCCCTATTGGCGATGGCGCGCAGATGGCGCCTGGACCGATCTTGTGCGCGTTGCGG
ACGGCGACGCGGTGGGTGGTCAAGTCCGGTCTACGCTTGGGCTTTGCGGACGGTCCGACGCTGGTCGCGGTTGCGC
CGCGAAAGCGGGGTCGGGTGCCATCAGGAATGCCTACCGCCGCGGCACTGCACGGCCAGTGCCCGCGGATGTCA
GCCATCGGGACATCATGCTCGGTTCTACTCTCGACAGTCGGCGGAACAGCTCGATTCCCGGACCGCCAGCGCA

TTGGTGATGGAATCGGCGAACTTGGCCACCCGCTGGGTGTTGACATCCTCGACGGTGGGCAATTGCCCCGGTAACGT
TTGCCGCCT. (SEQ ID NO. 182)

.....:Rv191T7.seq:.....
CGGTCCGACCCTGTTGACGGCTACCTGAATCAACCCGATGCCACCGCCGCGGCGTTGACGCGCGACAGCTGGTACCG
CACC GGCGACGTCGCGGTGGTTCGACGGCAGTGGGATGCACCGCATCGTGGGACGCGAGTGGTTCGACTTGATCAAGTC
GGGTGGATACCGGGTCGGCGCCGGTGAATTGAAACGGTGCTGCTCGGGCATCCGGACGTGGCGGAGGCGGCAGTCGT
CGGGGTGCCGACGATGATCTAGGCCAGCGGATCGTTGCCTACGTAGTCGGCTCAGCGAATGTCGATGCGGACGGGCT
TATCAACTTTGTTGCCCAACAACCTTCGGTGACAAACGCGCGAGGTGCGTATCGTANATGCGCTGCCGCGCAA
CGCCTTGGGGAAAGTGCTCCAGAACATTGCTGTCAGAAGCTGANCTACCGCAATTATCGTGTACGCTGGA
(SEQ ID NO. 183)

Clone Rv192

.....:Rv192SP6.seq:.....
ATACTCAAGCTTGGCGAAGTTCCGATGGGTGCGCGCGCGAGCCAGCGAAGTCGTACCGTGCGCGTGTCTTGGCT
TCGGATCTATCCTCGTTCATGACCGGCACCGTGTGGACGTGACTGGCGCGCGGTCCATATGACACCGAGATCATTGC
CACGGTACGGCAATTGTCGAAGAAGGAAATCTTTCCCAATGCACCGGCCCTCGAACGTGGCAACAGCTACCCGCAAGA
AATCGTCGATCGGCTGGGTGTTATTGGCTTGCTCGGTGCGCGGCTGCAAGGGTATCGACACCACCGAGTTTATTCTCG
GGCGTGCCGCGCATTCGAGCTGGCGGTGCGCGCTGCCAGCACCGTCATAGGTACTTGACGATGGTCCACGTCGGAC
GAGCGCTCCACGTCGCTGCCGAACGGTATGCATGGCGGCTACGATTCTC (SEQ ID NO. 184)

.....:Rv192T7.seq:.....
CGGTGTCGGCACCGCGTCTGCGAGTTGGTAGGCCTGCGAGTTTGTGCATCAGGCCGATGCCGCGGCCCTCGTGGCCAC
GCATGTACAGCACCGCGCGCCCTCACGGGCGACCATCGCCAGCGCGCGTCCAGCTGAGGCCCGCAATCGCAGC
GGCGTGACCCAAACACATCGCCGGTCAAGCACTCCGAATGCACCGGACAGCAGCTCGTCACCGTCGGCGTTGGGCC
CGGCGATCTCGCCGCGGACAGCGCGACATGTTCCACGTCCTCGTAGATGCTGGTGTAGCCGATGGCGCGAACTCCC
CATGACGAGTCGGAATCCGCGCCTCGGCGACCCGCTCAATGTGCTTCTCGTGCTTGCGCGGCCATTGATCAAGTCAG
CAATGGTGATCAGCGCCAGACCGTGCTCATCGGCGAACACCGCAATTCATCGGTGTTGCGCCATCGAGCCCTCATCTT
TTTGGCTGACGATCTCGCAAATCGCCCCCGCGGGTTGCAGCCGGCAT (SEQ ID NO. 185)

Clone Rv193

.....:Rv193SP6.seq:.....
ATACTCAAGCTTTGGGTGAAAGCCGATCACCGGAAGCCGATGATCAGCCACGTTTCGCGCCGCCCGGCATACGGCGG
CGTACCGATCTCCGCGTCATACACCCGCGGGTAATCGCCGACGGTGCCGGTTCGCGAGCCGAAGGTGACGACGCTGAT
TGAATCGAGTTCCAGGTCCAGCGGGTGGCGCAGCAACGGCGGAGCTCAACGACGTCATCAGGTTGTCGCTTTCTAC
GGTCACCGACCCGGTGACCGTNCCTCGCCCGGTGCGCTCGGCCGATAAGTTGCACCGCCACCACCGCGACACCGTCTTG
CACGCGGACCCACCCCGGATCCGTTGTTGGCC (SEQ ID NO. 186)

.....:Rv193T7.seq:.....
AGCTTGCTGGCATCCGCTCCAGTAGCGCCCCGCGGTGGCTTCCAGCGCCCGCAGATGCTCCATGAGCCGGCCGGTTCG
AGTCGGCGCCGGCGTTACCGCCACCCGCCAGGAGTGGCGGCCAGCATCTCCGCCCTCAGGCATTGCGCGATCACAG
AGAGAATATACGTCTCATATTGTTGGAGGTGCTCGCAGGCAATCGGTGATGACGGATTTGATGGCATCGAGCTGTG
CTTCGGCGTAGCCCTCCAGCACGTGCGGTATCGCTGTGGCGGTCCACGACGACCGCACCGGCGCGGCGGACAGCCGTCG
GGTTGGACGNTGTGCGCGCATCAGTCCGGCCAGTCCGCCCTCGGGATCAGCGGC (SEQ ID NO. 187)

Clone Rv194

.....:Rv194SP6.seq:.....
ATACTCAAGCTTGCTGCGAGCTTCCTATGACTGCTCCGAAACCTGGGGGTGTGCCTGCTGTGTATGCACGGCATAACGG
ACATCCTTCCCCTGAGACCCGCGGTGCAACCAGCCACGTGTCCATCATCAGGGGTCAACCCCGGCCAAGGGCGACGGC
ACGCCAAGTTGCGCGACCGTTAACCTAGTGCTGTAGCTTCATTTGCTGCGAGCAAAACAGCTGGTGGCCGCTTAGGA
ACTGAATTGAAACTCAACCGATTTGGTGCCGCCGTAAGTGCTGCTGGCTGCGGGTGCCTGCTGGTGTGTCGCGTGTGGT
AACNACNACAATGTGACCGGGGGAGGTGCAACCACTGGCCAGGCGTCGGCGAAGGTGATTGCGGGGGGAAGAAGAAC
TCAAAGCCAGTGGGTGACGCGCAGGCCAACGC (SEQ ID NO. 188)

.....:Rv194T7.seq:.....
AGCTTGACGCGGAGACGGACACATTGCGAACATTGATGACAAAATAGAAATCATTGATGGTTTGAGTCACCAGGCCGA
TCAAGCCTTTCGCCGAGCCAAATTCCAATCAAGAGGCCCAAGCCGTAACCAATCAGCCCGGCAACGAGGGATTCCGTCA
TTATCAGCCAAAATAACTGCTCTCGGGTTACACCCAAACAGCGCAATATGGCGAAAAACGGTCGCGCTTGACCGACAT
TAAATGTCACGGTATTGTAGATTAAAAAGATACCCACCAACAAGGCAATCAAATGAGAGCGGTTAAATTGACCGTAA

AAGCGTCCGTCACTCTGTTGACGGTGTCCCGTTGGGTATCCGACGTTTCCATACGCACACCGGCCGGCAGTCTTTGTT
GGATGCGTGTGTCAGTGGCCTCATCTTTGATGATCAAATCGATGTGGCTCAGTCTTCCGGGCA (SEQ ID NO. 189)

Clone Rv195

:Rv195SP6.seq:::

ATACTCAAGCTTCGGCTCAGGCGGCGCTGCTGGTAAAGTCGCTGACCGGTGCAGGTTTCGACAATGTGGTGCCGGTTC
GGCGGCTACGTGCCATCGAGACACTGGCGCAGGCTATCGCACCCGTTATCGGCTACGAGCAAATCGCGGTATGCGTTC
TTGAGCATGAGTCGGCGACCGTCGTATGGTCGACACCCACGACGGAAGACGCAGATCGCCGTCAAGCATGTGTGCC
GCGGATTATCAGGACTGACCTCCTGGCTGACCGGCATGTTGGTCGCGATGCCTGGCGCCCGGCCGGCGTGGTCGTGG
TCCGCTCGGATAGCGAGGTCAGCGAATTCNCNTGGCAGCTCAAAGGGTCTGCCGGTGCCGGTCTTTCGCGAAACNA
AGGCNCAGGTTA (SEQ ID NO. 190)

:Rv195T7.seq:::

TGATCGCGCATCACCTGCTTCATAAACTGGAAGCAGCGCAGCGCTTCCTTTTCGGCCGCAACATGAGCCAGCCTCTCG
TCGGCGGTTCGGGTGCAGGTGCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCCCTGAAACCAGCTTCCATATCCCGCG
ACGAACGACGCCAGTCCGCTACGTAACCCCTCCGCGCATGTTCCATGGACAACAGCGCGTCTCCACCGACCGGGCCCG
GGTGTGGGTGTTTCGGCGACCGGCAGCCAGGTGGTCCCACTGCCGACGGCGCCGCGAGCCGTTACCGACACAGGC
CGCCGAGCAAGTCCGCCCAGTCGCATACTCCAACCGGTTGCGGTACTGCAGGTTAGCTGGCGTACTCCTCGTCGCGC
TCGGCGAGGTCTTGCTCCAGCACGTGCGANACGGCAG (SEQ ID NO. 191)

Clone Rv196

:Rv196SP6.seq:::

CAAAGCGCAACTGCTCGCGGCAGCCACGACGTGCTGCGTCGGATTGCCGGCGGCGAAATCAATTCCAGGCAGCTCC
CGGACAATGCGGCTCTGCTGGCCCGCAACGAAGGACTCGAGGTCACCCCGGTGCCCGGGTTCGTGGTGACCTGCCGA
TCGCAAGGTTGGCCCAACAACCGGCCGCTTGATGCCCGGTTCGGCAAGCCCGGAGTTGCCAAACCCAGCGTGATCAGG
CTCGGCTCGCGAGTTCGGGAAGAAGTGGCTCCGCTGATCACCTACCATCCGCCAGGATCTGCGTGTCTTACCACG
CCCGCCAAGGAGGTTGTTGTGGTGCTATCGACCGN (SEQ ID NO. 192)

:Rv196T7.seq:::

CCGGAAGCCGCATGATCAGCCAAGTTTCGCGCCGCCCCGGCATAACGGCGGTACCGATCTCCGCGTCATACACCCCGG
GGTAATCGCCGACGGTGCCGGTTCGCGAGCCGAAGGTGACGACGCTGATTGAATCGAGTTCCAGGTCCAGCGGGTGGC
GCAGCAACGGCGCGAGCTCAACGACGTCAATCAGGTTGTGCTTTCTACGGTCACCGACCCGGTGACCGTNGTCGCC
GGTGCGCTCGGCCGAAAANTTGCACCGCCACCCGCGAAACCGTCTTGACNCCGGAAGCCACCCCGATCCGTTGT
TGGGCCAGGTTATTGGGT (SEQ ID NO. 193)

Clone Rv19

:Rv19SP6.seq:::

CCGGAACCGCCGACGGCACGGTATAACGCCTCCGTCATGCGGTGACAAACAGCGGGTCGGACTTCTGGGCTTCTAGC
GTTTCGCGCNGTCGCGACAAACAGCGCGGTGCAACCGACACTCGTTGTGATGTCCTAGCTATCAGGTTCCGTACGCACC
CAATCGAGTCTAGCGCGGTAGNTCAGCCCCGATCTCCANGCTCCGCCGAGCCAGGCGC (SEQ ID NO. 194)

:Rv19T7.seq:::

CTGGTTTATGTCCTGTTGAAGTTCATCACCCGATGTGGCGGGAGCACTGCCAGGTCGATCTCAACTACCACATCCGG
CCGTGGCGGTTGCGCGCCCCGGGGGTTCGGCGCGAACTCGACGAGGCGGTTCGGAGAAATCGCCAGCACCCCGCTGAAC
CGCGACCACCCGCTGTGGGAGATGTACTTCGTTGAGGGGCTTGCCAACCACCGGATCGCGGTGGTTGCC

(SEQ ID NO. 195)

Clone Rv1

:Rv1SP6D2.seq:::

CCGAGCAGTTGGGAATCGCTCTGCANCAACCAATATTCTGCGCGACGTGCGCGACGAGCTGGACCGATTAGGCGTA
CGCTCCGNTGGACGACACCGGGGCACTCGATGACCCCGACGCTACGCTCGCAGGATATTGTTCCCGGACCCCTC
TCTAG (SEQ ID NO. 196)

:Rv1T7.seq:::

TATATAACTCAAGCTTGCCGACGCCAACGCTCGCGCGATGTTGTTAGCCCGACCCGGCTCTTACATGGCACCGGTG
CCCCACAGTCAGCCTGTGACGTCCTGCACCGGACTCTTACATAGAATGTGGATTGCCGGATTGGGGATGTCCGGC
ATCGCTCAATCTGTAGTCCGCGTTGTCCCGGAGGGCCATGTGGATGGGGGAAGGATCCGTGGCGTCCGGGATCACC
ATGGGG (SEQ ID NO. 197)

Clone Rv201

:::Rv201SP6.seq:::

ATACTCAAGCTTGCCGAAGTTCCGATGGGTCGCGCCGGCGAGCCCAACGAAATCGCTAGCGTGGCCGTGTTCTTGGCT
TCGGATCTATCCTCGTACATGACCGGCACCGTGTGGACGTGACTGGCGGCCGGTTCATATGACACCGAGATCATTGC
CACGGTACGGAAATTCGTCCAGAAGGAAATCTTCCCAATGCACCGGCCCTCGAACGTGGCAACAGCTACCCGCAAGA
AATCGTCAATCGGCTGGGTGTTATTGGCTTGCTCGGTGCGCGGCTGCGAGGGTTTCTACACCACCGAGTTCATTCTCG
GGCGTGCCGGCGCATTCGAACTGGCGGTGCGCGCTG (SEQ ID NO. 198)

:::Rv201T7.seq:::

GCACCGGCGTCTGCAAGTTGGTAGGCCTGCAAGTTTGTGCATCAGGCCGATGCCGCGGCCCTCGTGGCCACGCATGTAC
AGCACCACGCGCGCCCTCACGGGCGACCATCGCCAGCGCGGCGTCCAGCTGAGGCCGCAATCGCAGCGCGCTGAC
CCAAACACATCGCCGGTCAAGCACTCCGAATGCACCGGACAGCACGTCTTACCCTCGGCGTTGGGCGCGGCGATC
TCGCCGCGGACCAACGCGACATGTTCCACGTCTCGTAGATGCTGGTGTAGCCGATGGCGCGAACTCCCCANGACAA
GTCGGAATCCGCGCCTCGGCGAACCCTCAATGTGCCTCTCGTGCTTGCGCCGCCATTC (SEQ ID NO. 199)

Clone Rv204

:::Rv204SP6.seq:::

TGGTCCGTGTGCGCATACCAATACAACGCGCGGGCACCTGACGCGGCGGCCGCAACCAATCGGTGGCCATCGCCATC
TTCTGCTACCCGGTCAACGGACGCACCTTCTCCTGGCCGACGTAGTGCGCCACCCGCCCGCTTGGTCCCATCGAT
CCGGTCAAC (SEQ ID NO. 200)

Clone Rv205

:::Rv205SP6.seq:::

GGCGTGTGGCCACCGGGGCCACTCCGCACAATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTCGCC
GACTTCCGCGGTACCCGCTCAACTTTGTGTGCGACCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAACCTAC
TTCATCCTGACGCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGACCCAGTACTAC
ATCATTCGCACGGAGAACCTGCCGCTGCTAAAGCCACTGGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCT
GGTTCAACCAAACTTGAAGTGATTGTTTACCTGGGCTACGGCGACCCGGCCTATGGTTATTGACCTCCCCGCCCAA
(SEQ ID NO. 201)

:::Rv205T7.seq:::

CGTCCGTGNCCCTCAANCGCGTGNNGCCGAAGCGGCTGGTTACGACTCCCTGTTTGTGATGGACACTTCTACCAACT
GCCCATGTTGGGGACGCCCGACCGATGCTGGAGGCCTACACGGCCCTTGGTGGCTGGCCACGGCAGCCGANGC
GCTGCAACTGGGCGCGTGGTGACCGGAATACCTACCGCAGCCCGACCTGCTGGCAAAGATCATCAACACGCTCGA
CGTGGTTAGCGCCGGTCGAGCGATCCTCGGCATTGGAGCCGGTTGGTTTGGAGCTGGAAACACCGCCAGCTCGGCTTCG
AGTTCGGCACTTTCAGTGACCGGTTCAACCGGCTCGAAGAGGCGCTACAGATCCTCCAGCCAATGGTCAAGGGTGAGC
GCCAACGTTTTTCGGCGATTGGTACACCACCGAATC (SEQ ID NO. 202)

Clone Rv207

:::Rv207SP6.seq:::

CCGCTTCCGTGTAACCGAGCANNGCAGCGANCTGGCGAGGAAGCAAAGAAGAACTGTTCTGTGATAGCTCTTACG
CTCAGCGCAAGAAGAAATATCCACCGTGGGAAAACTCCAGGTAGAGGTACACACGCGGATAGCCAATTCAGAGTAAT
AACTGTGATAATCAACCCTCATCAATGATGACGAACTATCCCCGATATCAGGTACATGACGAAGGGAAAGAGAAG
GAAATCAACTGTGACAACTGCCCTCAAATTTGGCTTCTTAAAAATTACAGTTCAAAAAGTATGAGAAAATCCATGC
AGGCTGAAGGAAACAGCAAACTGTGACAAATTACCCTCAGTAGGTGAGAACAAATGTGACGAACCCCTCAAATCT
GTGACAGATAACCCCTCAGACTATCCTGTCGTGATGGAAGTATATCGCGGAAGGAAATACGATNTGAGTCGTCTGGC
GGCCTTTCTTTTCTCAATGTATGAGAGCG (SEQ ID NO. 203)

Clone Rv209

:::Rv209SP6.seq:::

TGACACCCAACAGAGGGCACTTAAGATGGCAATGCGGCCGCTACCTGCACGTTTTCGCGATGTCAGAGGATGCCGAG
GGAGAACAATGCGAGCACGGCCGCTGACNTTGTCAACGCTTTGGCGCGGCGTACATTGGTGGTGGTGGCGGCTGCN
AGGCCCGANTCNAGCCGAAGCATATAGCGCGGCCGACCGCATTCGTCTCGACCGCAAGCGGACCTCAGCCGCAGC
CGGTGGAGCTACTGCTGCGCGCCATCACGCC (SEQ ID NO. 204)

:::Rv209T7.seq:::

ACGGGCGACGCTGAGGTGGGCGCGGCTATTATGCTGTGCTCCACGTCCAGCGACGCACTGCGCCAGACGGCCCGC
CAACTAGCCACCTGGGTGGAAGAACACAGGACTGCGTGGCGGCTCGGATCTGGCCTACACGCTGGCGCGTGGCCGC
GCGCACCGGCGGTCGCGACCGCGGTGGTTGCGCCAACCTGCCGGAGCTCGTCGAGGGTTGCGCGAGGTGGCCGAC

GGTGACCCCTCTATGACGCGGCGGTGGGACACTGTGATCTAAGACCGGTCTGGGTCTTCTCCGGGCAAGGGTCTCAGT
GGGCGGCGATGGGCACCCAATTGCTCGCCAGCGAACCAGTGTTTCGCGGCCACCATCG (SEQ ID NO. 205)

Clone Rv20

.....Rv20SP6.seq:.....
ATACTCAAGCTTCGCGAGATCCGGATGGCACTCACGCTGGACAAGACCTTCACAAAATCTGAAATCCTGACCCGATAC
TTGAACCTGGTCTCGTTCGGCAATAACTCGTTCGGCGTGCAGGACGCGGCGCAAACGTACTTCGGCATCAACGCGTCC
GACCTGAATTGGCAGCAAGCGGCGCTGCTGGCCGGCATGGTGCAATCGACCAGCACGCTCAACCCGTACACCAACCCC
GACGCGCGCTGGCCCGGCGGAACGTGGTCTCGACACCATGATCNAAAATCTCCCGGGAGGCGGAGGCGTTGCGTG
CCGCCCAGGGCGAACCGCTGGGGGTTCTGCCGCAAGCCCAATGATTGCCGCGCGGTGCATCGCGGGCGGCGACCGCCA
TTCTTCTGCGAATACGTCCAGGAGTACTGTCTCGGGG (SEQ ID NO. 206)

.....Rv20T7.seq:.....
AGCTTATGTGGCCGCCACCTACCTTATCTAGCCTAGCTAACTAAATCCAGTGCCGACAGTGCGCGGTGGCCACCCA
GCATGAGGTTATGACCACGGCATATGCCAGCGCGTGGCGGCGATGCCGACGCTGACCGAGTTGGCCGCTAATCACAC
CAGCCATGCGGTGTTGCTGGGAACGAATTTCTTTGGAATCAATACGATCCCGATCGCGCTCAATGAGGCCGACTATGC
GCGGATGTGGATTGAGGCGGCCACACGATGAGTATCTATGAGGGCACCTCCGATGCGGCGCTGGCGTCNGCACCGBA
AACCACACCGGCTCCGCTACTGTTCAACGGCGGTGCTGGCGTTTGCCAGCGCCTGCCGGCGATCTC (SEQ ID NO. 207)

Clone Rv214

.....Rv214SP6.seq:.....
ATACTCAAGCTTGCCACCCATGCCGAGCAAGGTCGACTCAGCGATGACGAATTGTTCTTCTTCGCGGTGTTGCTGCTG
GTTGCGGGCTATGAGAGCACTGCTCATATGATTAGCACNTTGTCTGACGCTGGCCGACTATCCAGATCAGCTGACA
CTCCTTGCGCAGCAACCAGACCTGATCCCGTGGCGATCGAGGAGCACCTCCGCTTTATATCGCAATCCAAAACATCT
GCCGCACAACGCGCGTCACTATTGCGTGGTCAAGCGGTCAATCCCGGGA (SEQ ID NO. 208)

.....Rv214T7.seq:.....
CCGGGGTAGAACGATGCGATCTGGGCCATGTCGACATCGGTGGTACAGGTAAACCGCGCCGTGTGCGCGGTCTCGGAG
ATCAGAACGTGGTTCGAGTTGACACCGCGGGCTTTCAGCCAGTCGCGATAATCGGCGAAGTCGGCGCCTGCCGCCCA
ATAGCGCGACCTCGCCACCTAGCACACCGATGGCGAAGGCCATGTTTCGGCCACGCGCCGCGGTGCATCATCAAC
TC (SEQ ID NO. 209)

Clone Rv215

.....Rv215SP6.seq:.....
ATACTCAAGCTTGGCGGCAACGCCACTACCGGGCTCACCAGGTCTGTGCCGCCACCGCGGCGCCGAAAGCACCATC
AGGTCGTAGTTGTCTGGACGTTTCGACACCGTAAGCGAACAATGCCGCCGCCATGCTGTGCCCGAGCAGATGCGC
TTGCACCCGGGATATTCCCGGTGGCGATCCCAACGAGGGTGTGCAAGTCAGCGGTGTATCTGAGATGTCTCTACTA
TCATCCGTTTGGCACCCGAGCGGGCATGCCCGGGGGGTCAAC (SEQ ID NO. 210)

.....Rv215T7.seq:.....
GTCGACGGCATCAAGGTCCGCAGTGATGGTGTTATCTCACCCAGGAAGGCGTGAAGTGGCTGATACCGTGGCTTGAG
GATTCGGTGGGGTCGCCAGTTAATCCGCCGTGTGCTCCGGATGAGCGCGACGGTAACCTGGAATTGTGCTGTGTGC
TGGCTGTGTCGTTGTGATGAGCCTGTCTAAGTGGTGCCTAACCGTTTGACGAGCCGCGGCCTCGCTGCAAACATTGAA
GCCCGCACGTCTGGGTTGTATTTACACAACGAGGGCGCTCCCCGATCTGGCGCGCGCAACGAGGTGCNCACTATCCA
TTCGAGGTGAAGTGGACTCCTTGATGCTCATGCCGTTGCGGTTTGTGTC (SEQ ID NO. 211)

Clone Rv217

.....Rv217SP6.seq:.....
ATACTCAAGCTTGCCTTCGATGAAGTAGTCGTGGTCAGCGCCGCTCTTCGAGCTCCTTGGCGATGCCAGCAAGGA
GTCATCGCCGCCGAGCTTGGCCAGGATCTTGTCCGCTGCTCGACCGCCCTTCTTACGATGCGGGCCCGGATCGTAGTTCTTGTA
GACACGATGACCGAAACCATCAATTTGACCCCGGCTCGCGGTTCTTGACCTTGCGTTACAAACTCGCTGACGTGCGT
CGCCGCTGTGCGAATGCCCTC (SEQ ID NO. 212)

.....Rv217T7.seq:.....
NGTCAAGCCGAGCATGCGCGAGGNAACGACGAACCAAGCCATGGTGGTTGGCGCCGTGAGAGGTGCGCGGTGCG
CCACAACGGGAAGATCGCCTTGAGCGTCGCTCGACCGCCCTCGAGTTGGGTACATAACGAAGTAGCTGATGCCGATC
ATGTGACGTTTCCGTGCGATCAGCGTGCAGCGCGCACCCACTCGACGAGGTCTCGGTGCCCGCGCGGCCAGGGCACC
AGCAGTGACGATTCCAGGCGCGGTGCGG (SEQ ID NO. 213)

Clone Rv218

.....Rv218SP6.seq.....
CGATAATCGCTTCCGGTAAGTGCAGCAGCTTTACGACGGCGACTCCCATCGGCAATTTCTATGACACCAGATACTCTT
CGACCGAACGCGGTTCTGTTGACCACTCAGTAGAAAAGAAGGGATGAGATCTCCCCGTGCGTCTCAGTAAGCAGC
TCCTGGTGCAGTTCATTACCTGACCATACCCGAGAGGTCTTCTCAACACTATCACCCGGAGCACTTCTAGAGTAAAC
TTCCCATCCCGACCACATATAGGCTAAGGTAATGGGCATTACCGCGAGCCATTACTCCTACGCGCGCAATTAACGAAT
CCACCATCGGGGCGGCTGGTGTCTN (SEQ ID NO. 214)

Clone Rv219

.....Rv219SP6.seq.....
NAATACTCAAGCTTTCTCGTGATTACCAACCGTGTAATTTGGGATGGGCAAAAAGGCGAATCACCGCGTGGCCACAAA
CGCCGGGAGGGACAACTCTCGGGCGGCTAGGGCTTCTCGCGGAAGGCCCGAACGTACGGCGTTTCAACACGTCGCGTC
GCCCTCCGACCGCGAACATTGCGGGATGGCAGCAACCTGGTATCACCTGGCCGGGCAATGATCTGCAGCGTCGCCGC
GGGTAGTGNCCGCGCGGCGGCTAC (SEQ ID NO. 215)

.....Rv219T7.seq.....
CCAAGTAGAGCATCGGGACATACGGAGTCAACTACCCGGCCAAACGGTGATTTCTTGGCCGCGCTGACGGCGCGAAGC
ACGCCAGCGACCACATTCAGCAGATGGCCAGCGCGTGCCGGGCCACGATGTTGGTGCTCGGCGGCTACTCCCAGGGTG
CGGCCGTGATCGACATCGTCACCGCCGACCACTGCCGGTCTCGGGTTCACGCAGCCGTTGCCGCCGCGAGCGGACG
ATCACATCGCCGCGATCGCCCTGTTGCGGAATCCCTCGGGGCGCGCTGGCGGGCTGATGATCGCCCTGACCCCTCAA
TTCGGGTCCAAGA (SEQ ID NO. 216)

Clone Rv21

.....Rv21SP6.seq.....
ATACTCAAGCTTGCTGCAGCTTCTGTGACTGCTCCCGAAACCTGGGGGTGTGCCTGCTGTGTATGCACGGCATAACGG
ACATCCTTCCCTTGAGACCCGCGGTGGAACAGCCACGTGTCCATCATCAGGGGTCAACCCCGGCCAAGGGCGACGGC
ACGCCAAGTTGCGCGACCGTTAACCTAGTGCTGTTAGCTTCATTTGCTGCGAGCAAAACAGTGGTCGGCCGTTAGGA
ACTGAATTGAAACTCAACCGATTGTTGCTGCCGCCGTAAGTGCTGCTGGCTGCCGGTGCCTGGTGT
(SEQ ID NO. 217)

.....Rv21T7.seq.....
AGCTTGCGCGCGTGGCGATCGCGTTCAAGGCGCGCTCTTCGAGCACAAACGAGCGAAGACAGCTCGGCGACGGAGCC
TTTATCGACATCCGTTGCGGGTGGCTGACCGGCGCGGAAGAACTGCTGGACGCGTGTGTGTCGACGGTGCCGTGGCGA
GCCGAGCGCGTCAAGTGTACGACCGGTGGTCGATGTGCCGCGGTGGTGAGTTTTACGACCTGACCATCGAAGAT
CCGCCGATCCGACGCTGGCGCGGATGCGCC (SEQ ID NO. 218)

Clone Rv220

.....Rv220SP6.seq.....
AATACTCAAGCTTGCGCACGACAGGACGTCGAGTGGCGCTTGCACTGACTTGCGGACCTCAAAGGCCACCGGTACCC
CGCCGCGCGCAAGCCAAGGACNACNACGGCTTGCCGGATAGTGCGCCAGGCGTTGCGCCAAGTGGCGTCCAGCGT
CGCCACGATCGTCAAAGAGCTTCATCTGCCAGTGTGTGCCATCTCATGGCTCCAAATATGGAATTAGGTCCCTGGG
CCGACTGACGACAGTCCCTCAGCGACCGGATTGCGCATCCCGCTTGTACGCTGCTCCGCAATCCCGGGCTTGGCTC
CGCGAAGCGAACTCGGCGGCGCTACGGTGGTGGCTCACTTCGGCCGTG (SEQ ID NO. 219)

.....Rv220T7.seq.....
GGTGGTGCGGTCCACCTTCGCGGCGGCGCGCATATGCCTTGCTGGTCTTGCTCATTTGATATCCAATCTATGGGT
CGTGGTTACTCAGCGGGCCGAAGCTGGCCCTCCACGGGTAGGGCCCTATTGACGGTGATGCCATCGACCGAGCGG
TACCGCGGATGATCTTGCCGCGAGCGTCGACGTCGTTGGCGTTGAGGTCCGTCTTCTGGTCTCGGCGATTTGCGCGA
CTTGATCCCAGGTGACTTTGGCGACCTTGGTCTTGTGCGGCTCCGCCGAACCTTCGCCACACCAGCGGCCCTTAAGCA
GCAGCTTGCGGCGGGCGGCGTCTTCAGCGTGAAAGTGAAGTACGGTCTTCATAAACGGTGATCTCCACCGGGATGA
CGTTGCCGCGTGGTCTCCGTCGCGGCGTGTACGCCTTGCAAGAACTCATGATGTTGACCCGTGCTGACCGAAGCG
GGGCGCACTGGCGGGG (SEQ ID NO. 220)

Clone Rv221

.....Rv221SP6.seq.....
ATACTCAAGCTTTTCGACCCGAAGCGGCGGTGCCCTCCTCGTTCGCGTGGCCGGTCTGCTCGATCGGTTTCGGGGT
CGCCGCGCTAGGCCCAATTGCCCGGCTCCTCCTCGGGCGGTTCCACAACCCGATCGTCGCGGGCTAGGTTCAAGCC
ATGCCGGTAAACCCAGGACGCCAGTGCTGATCGGCTATGGACAGGTCAACCAACGAGGCGACATCGACGCCNAAAAAT

CAGTCCATCGAACCCGTCGACCTGATGGCCNCCGGGCCCGGAAAGCCGCCGAGTCCACCGTGCTCGAAGCGGTGGAT
TCCATCCGTGTGGTGCACATGCTGTCGGCGCATTAACCGGAATCCCGGGCGTCTCCTCGGC (SEQ ID NO. 221)

::::::::::Rv221T7.seq::::::::::
NCCTGGTTCATGAACTGGAAGCAGCGCAGCGCTTCCTTTTCGGCCGCAACATGAGCCAGCCTCTCGTCGGCGGTTCGGG
TGCAGGTGCTCGGGCAGCTCGGCCGCGACGCCGCTGACCCTGAAACCAGCTTCCATATCCCGCGACGAACGACGCC
AGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACAGCGCTTCTCCACCGACCGGGGCCGGGTGTTGGGGTG
TTCGGCAACGGCAACCAAGTTGGTCCACACTGCCGACGGGCGCCGCAATCCGTTACCGAACCAGGCCGCCNAAACA
ATTCCGCCCCGATCCCATAT (SEQ ID NO. 222)

Clone Rv222

::::::::::Rv222SP6.seq::::::::::
ATACTCAAGCTTGTCCGGATCAATCTCGAGGGCATCCACGCACGAAAAGTAACTCTATCAAGCTTTTTGACGACACC
CACGGACGCCCCATATATGTTCCGGTGGGCAAGAAGGTCCCTACCTGGAACGTTTGGTGGCCGGCGACACCGGTGAG
CCCACGCCGCGACGGGCCAACCTCAGCGACTCGATTACCCCGACGAACCTGACTCTACAGGTGGCCGAAGAGCTCTTT
GCCACACCGCAACAGGGACGGACTTTGGGCTTGGACCCAGAAACCGGCCACGAAATCTTGGCAGGGGAAGGCCGGTT
TGGGCTTATGTTACCTATATCTGCCGGAACCTGCGGCTGATGCGGCCGCGGCCGCTCAGGGAN (SEQ ID NO. 223)

::::::::::Rv222T7.seq::::::::::
AGCAGCTAGCCGCGCTCGCCGCGCTGGTCCGGTGCATGCTCGCAGCCGGATGCACCAACGTGGTTCGACGGGACCG
CCGTGGCTGCCGACAAATCCGGACCACTGCATCAGGATCCGATACCGGTTTCAGCGCTTGAAGGGCTGCTTCTCGACT
TGAGCCAGATCAATGCCGCGCTGGGTGCGACATCGATGAAGGTGTGGTTCAACGCCAAGGCAATGTGGGACTGGAGCA
AGAGCGTGGCCGACAAGAATTGCCTGGGCTATCGACGGTCCAGCACAGGAAAAGGTCTATGCCGCGACCGGGTGGACC
GCTATGCGCGGCCAACGGCTGGATGACAGCATCGATGACTCCAAGAAACGCGACCACTACGCCATTCAAGCGGTCTGTC
GGCTTCCCGACCGCACATGATGCCGAAGAATTCTACAGCTCCTCCG (SEQ ID NO. 224)

Clone Rv223

::::::::::Rv223IS1081N1400.seq::::::::::
CGCGACTGGCTCCCCGGNCGGCTGCTCGGGTCCGCCGATAGAGACCGGGATGTGCCCCGACGACGGGCAGCCGGGTTG
CGTGGGACGGGGCGGGGGTTCGGGCAGCCCAAGCAACGGGCTAGTCCCCGAATCCTACGGAGCCGTACCTACGCCTAC
GTAATAGTAGCTATCAATAACAGTTGACATACGCCAACGATCTGTGAGATCAATATTGCCTGACGCATGTCAAGACAGG
CGTCAAGACAGGTGTCAATAATTCCGCTCCGCTGGTGACGGTAACCGGTCGTGCGGGTGTGTGACGCCAAGGAAGGAG
TGTGGGTGGTGACGCTGAGAGTGGTTCTGAGGGTTTGGCGGCCGCCAGTGCGGCGGTGGAGGCGTTGACCGCACGGC
TGCCCGCCGCACACGCTGGCGCGGCGCCGGCGATTACGGCGGTGGTGGCGCCCGCGGCGGATCCGGTGTCTGTTGCAGA
ATGCGGTGGGGTTTAGCGCCTTAAGTAGCCAGCATGCCGCGATCGCCGGCGAAAGGGTCCAAGAACTGGGT

(SEQ ID NO. 225)

::::::::::Rv223SP6.seq::::::::::
ATACTCAAGCTTATTGAACCGCGGTCGCGAGGCAAGTGGACCTCATAACGACTCGGGTCCAGCGACCGCGCCAACAC
GAACGGCCGGACGACGTGGGCCAGGGTCGCGGCTCCCTACAAACAGGATCCGTTGCCGCGAAGCAGGCTCCGG
TGCGGCGTTGGGCGCCGTGCTCGTCCCAGCGTCCGGTCCCGGTCGCCGGCGACGCTTGTTCCTCCATACCTGCCCC
CTAATCTCGAGGCAGCCGTACCCGCGAGGCAACCTCCAAAAATGCAATCCCGCAAAATGCAATGCGTCNAGCTATTT
CTCACACCGACCGTAGTTGCGGATCAGAAATCCGTTGGGCGCGGAAGTCCAGCCGAATTTGTTCTCCGCTCCGCAT
CATGCTTGTAATCGTTTGAAATTCATCCTCATATGCCTCGATCGCTTCATAGGGTCCAGGCCCAAACCCGGGCAGGA
CTGGGTGGCCGTTGATGTTGGAATCCTCCACTACTAGGTATTACCGGC (SEQ ID NO. 226)

::::::::::Rv223T7.seq::::::::::
GTCTCGATCATGGCCAAAGAGCTCGACGAAGCCGTAGAGGCGTTTCGGACCCGCCGCTCGATGCCGGCCCGTATACC
TTCCTCGCCGCGACGCCCTGGTGCTCAAGGTGCGCGAGGACGGCCGCTCGTCGGGGTGACACCTTGATCGCCACC
GGCGTCAACGCCGAGGGCTACCGAGAGATCCTGGGCATCCAGGTCACTCCGCCGAGGACGGGGCCGGTGGCTGGCG
TTCTTCCGCGACCTGGTCGCCCGCGGCTGTCCGGGTGCGGCTGGTACCGGCGACGCCACGCCGCGCTGGTGGCC
CGATCGGCGGCCACCTGCCGCGAGCGGCTGCGAGCGCTGCAAGCCACTACGCGAGCCAATCTGATGGCAGCCACC
CCGAAGCCCTCTGGCCGTGGGTGCGCACCCTGTGCACTCCATCTACGACCGCCGACGCCGAATCAGTTGTTGCC
AATATGATCGGGTCTCGAC (SEQ ID NO. 227)

Clone Rv224

::::::::::Rv224SP6.seq::::::::::
ATACTCAAGCTTTCGTGAGTTGATGCGCCAGCAGACCAACAAGAGCATCGGGACATACGGAGTCAACTACCGGCCA
ACGGTGATTTCTGGCCGCGCTGACGGCGCGAAGCAGCCAGCGACCATTCAGCAATGGCCAGCGCGTCCCGG

CCACGAGGTTGGTGTCTCGGCGGCTACTCCCAGGGTGC GGCGGTGATCAAGATCTTCACCGCCGCACTGCCCCGGCC
TCGGGTTACGCATCCGTTTGGCCGCCGCC (SEQ ID NO. 228)

.....Rv224T7.seq:.....
GCCCCGTGTAATTTGGGATGGGCAAAAAGCGAAGCACCGCGTGGCCACGAACGCCGGGAGGGACAATCTCGGGCGGCT
AGGGCTTCTCGCGGGAAGGCCCGAACGTACGGCGTTTCAACACGTGCGCTCGCCCTCCGACCGCGAACATTCTGGGGAT
GGCAGCAACCTGGTAGCACCTGGCCGGGCGATGATCTGCAGCGTGC GGCGGGTAGTCTCCGCCCCGGCCGC
(SEQ ID NO. 229)

Clone Rv225

.....Rv225SP6.seq:.....
ATACTCAAGCTTCTTTGACCGAACGCGTCCACCGCACCGTGAGATTGGTGGCGCCATTCTGTCGTGGTGTAGCTGCTG
TTGGCGCGGTGAGGCGTTTCGGCGAGGAGGTAGTGTCTACCCACAAGTCGGCACTTCCGCAACCG
CCCAGCTCGACCGCAATTACGGCGGGCCGAACGGCCGCCGGAAGGCGTCACGCAATCGCTTATCCTTCCAGGTTCC
CAATCTCCGCTTACTTGGGTCTTCATCGG (SEQ ID NO. 230)

.....Rv225T7.seq:.....
GGCAGCGGCGACAACCGGAACGTCCGCACGGTGCTCAATCACGGGTGCACGGTGTGCATCAGAATGGCGGGGGTTTCGT
TGTCGCGGTGAGGCGTTTCGGCGAGGAGGTAGTGTCTACCCCTTGCCCGCGGGTTCGTGCGGACTGAAAGGGATTTCAT
TGGGAACCCACGGCTGCGTATCGCAGGGCCTCGGTGACGTCTGCTTCCTCNAGCTCAGGAAGTTCGGCGAGAATCTCG
GTGGATGTTATTTGGTCCGCCTAC (SEQ ID NO. 231)

Clone Rv226

.....Rv226SP6.seq:.....
ATACTCAAGCTTCTCGGCTTCTCTGATAGCCTGAGAAGAAACCCCAAGTTAATCCGCTGCTTCACCTATTCTCCAGC
GCCGGGTATTTTCTCGCTTCCGGGCTGTATCATTAAGTGTGCAATGGCGATAGCCTTCGTATTTTCATGACCAG
CGTTTATGCACTGGTTAAGTGTTCATGAGTTTCATTCTGAACATCCTTTATTTCATTGTTTTGCGTT
(SEQ ID NO. 232)

Clone Rv227

.....Rv227SP6.seq:.....
ATACTCAAGCTTGGTGACCGGCACCGGATACGTTGCGGCAGGCATCTGGGCTGGCGGTGGTTCCGCGCTCCGAAGCC
GTCGAACACCATCGCCAGCGCGGCTTCCACATCAACGACCATTTCCGGCCAGCTTGGCGGCATCAGCGGCTTGTGAT
GAGCGCCCCACCGAATGCCCGCGCTGCCCGGCGTATCACATCGATTTCGACCATCGCGCGGCGCGGTTGCCGAGGGC
GAACGAGGCGGTGCCCAACCGCAATCTGTTTGGTCAGTCCCTCATGCGGGTTGATTCTTGCCGTCCGGACGGGCC
GCGTCATGCGCTCGGTTGCC (SEQ ID NO. 233)

.....Rv227T7.seq:.....
CCGTTGCGCAGCGTGAGCCGATAGTTGACATCCGGCTCGGTGAAGGTGAAATCGATGGCCAGGTCGAGGTCCCATGCG
CGTGGGCCATTGATGCTGATCGCCAGGACGTCAAAGATTTGGTCCGGCGTCAGCTGGGCGAAAAACGTGGGCGCCGGG
ACTTGCCCGGAGCTGCCGGGTTCCCGTCCGCGAGCTCGGCGGCCCCGGTCAGAAAGAAATTGCGCCAGGTCGCACAC
TCCGCGCCGTAGGCCAGCTGCTCCAGGGTGTCCGCATAGAGCCCCGGGCGCAGCGTGTCTGCTGTCGGCGAACACC
GCATGGTCGAGAAGCGTTGCCGCCAACGGGAATCACCTGCGTTCGAAAGCTTCGCGGGCCAGCTCCAGCACTCGGT
GATGCCACCAACGCGT (SEQ ID NO. 234)

Clone Rv228

.....Rv228SP6.seq:.....
ATACTCAAGCTTGGCGATGTTACCCCTGACAGCGTGAACATATGTCNAAACACACGGCACCGGAACGGTGTGGGGGAC
CCCATCGAGTTGAGTGTGTCGGGCCACTTATGGCCTGGGTAAAGGCCAGGGCGAGAGCCGTCGCGATTGGGGTCTG
GTCAAAACCAACATCGGCCACCTGGAGGCGGCGCCGGTGTGGCTGGATTTCATCAAGGCGGTGCTGGCGGTGCAACGT
GGGCACATTCCCCGCAACTTGCACTTACCCGGTGGAACCCGGCCATCAACACGTGCGGACGCGGCTGTTTGGTGGCG
ACCGAAAGCGCCCCGTGGCCGGCGGCTGCCGGTCCACGAGGGTGC GGTTGTCATGTTTCGCGCTCAGCGGGACCAA
(SEQ ID NO. 235)

.....Rv228T7.seq:.....
CCGGTAACAGATCAGCTCGTACCTCACTGCCGGGGTGAATTCACCGGTGCTGCGCGCTGCCAGTAGTGCA
CCTTCTTGACGCCTCGAAAAGGGGAGTCGGTGGGTAGGTACCGTCAGGAGCCGCCTACCCAGGTTGGCGCGGTGAC
CGGTCTCTCGAGTATCTCCGCAACCGCCCCACCGGTGCGGTCTCGCCCGGATCCACTTTGCCCTTGGGCAGCGACC
AGTCGTGTAACGGGGCGGTGAATGACAGCGATCTCGACCGGCCCTTCCGAATCGGCACTGCCGGGTGCCAGAACCA
CCGACCGGCGGCGTACACAATCCGGCCCGGAGCGCCGGGCGGACGANTTCTGGATCGACACCTCAACTCCTG
CAGGTCAATTCGGCCAAGCTGCTCGCGGTGCTGGATGTGGT (SEQ ID NO. 236)

Clone Rv229

.....Rv229SP6.seq.....
ATACTCAAGCTTGATGCCGCCGAAACCGAGCGTGAGCACGCCGCCACCCACACGCGCGGGTCGGGCGCCGGGCCCGG
GCCGCCAGGCTGCTCCGCTCGGTGATGGCAGCCACCGCGACACCACCCGGCTGCGCTACGTCGAGCCATACCGGGCG
GAGCTACATCGGCTCGGCCGCCAGTGTTCCGGGCCCTCTTTCGAGGTCGAGGTTCTATACCGATTTCGCGCATCCGCAGC
CGCACCTTGGTCTGCTACCGTGCCCTACCTCTGCTTGTGCGGGCGGGCCA (SEQ ID NO. 237)

.....Rv229T7.seq.....
TCCGTACGGCCCGGGTACGCTTCGGTCGCAGTGTGCGAGTGATAGATGACGACCGGGACCTCGTCGGCATCTTCCATA
GCCCCCACACCTTCAGTTGCTCACCAGGAATCCAACCGGTAGAGGTGCGCGAGCGCTCGGCATTGGTCATCGGGATA
TGCCGCTCGGGACGGTCAGAGCCCTCGGTCCGGCCAGCACTCCGCAGGCTTCGTGCGGGTGGTCGCGACGCGCATGG
GCCACCATCCATCCACAGGTCTGCGCAATCACCCGC (SEQ ID NO. 238)

Clone Rv22

.....Rv22SP6.seq.....
GGACACATTGCGAACATTGATGACAAAATAGAAATCATTGATGGTTTGAAGTACCAGGCCGATCAAGCCTTCGCCGAG
CCAAATTCATCAAGAGGCCCAAGCCCGTACCAATCAGCCCGGCAACGAGGGATTCCGTATTATCAGCCAAAATAA
CTGCTCTCGGGTTACACCCAAACAGCGCAATATGGCGAAAAACGGTCGCCGTTGCACGACATTAAATGTCACGGTATT
GTAAATTAAAAAGATACCCACCAACAAGGCAATCAAACCTGAGAGCGGTTAAATTGACCGTAAAGCGTCCGTATCTG
TTTGACGGTGTCCCGTTGGGTNTCCGACGTTTCCATACGCACACCGGCCCGGCGAGTCTTTGTTGGATGCGTGTTGCACT
GGCCTCATCTTTGATGATCA (SEQ ID NO. 239)

.....Rv22T7.seq.....
GCCTGGCCAGGTGAAGGCCGACCTCGACGCCAAAGCCGCTGATCCGGCACATGAGTCGGTGGACTGGGACTTGAAGT
CGCTGCGATGGGCGTGGAACCGAGCCAAAGATGACGTGGCGCCGTGGTGGGCCGAGAATTCCAAGGAGTGCTACTCGT
CGGGGTTGGCCGATCTGGCCAGGGCCTGGCTAATTGGAAAGCTGGCAAGAACGGGACCCGCAAGGCCGGCGGGTGG
GCTTCCCGCGATTCAAATCCGGGCGGCGTGATCCTGGCAGGGTGCCGTTTCAACACCGGCACCATGCGCATAGAGGATG
ACCGGCGCACGATCACGTTCCCGGTGATCGGGCCGCTGCGGGCCAAAGGAGAACACCCCGGGTGCAACGCCACCTCG
TGAGCGGGCGCGCGCAGATCCTGAACATGACCTTGTGCGAGCGTGGGG (SEQ ID NO. 240)

Clone Rv230

.....Rv230SP6.seq.....
TAACCTCAAGCTTCAAGTCCGCNGTCCGACCCTGTTTCGACGGCTACCTGAATCAACCCGATGCCCGCCGCGCGCTTCG
ACCCGACAGCTGGTACCGCACCGGCGACGTGCGCGGTGGTCGACGGCAGTGGGATGCACCGCATCGTGGGACGCGAGTC
GGTCGACTTGATCAAGTCCGGTGGATACCGGGTCCGGCGCCGGTGAAATTGAAACGGTGCTGCTCGGGCATCCGGACGT
GGCGGANCGGCGAGTCGTGCGGGTGCTCGACTATTATCTAGGCCAGCGGATCGTTGCCTACGTAGTCGGCTCAGCGAA
TGTCGATGCGGACGGGCTTATCAACTTTGTTGCCCAACAACCTT (SEQ ID NO. 241)

.....Rv230T7.seq.....
CCATGTCGCCCAACATATCGTCGATGTTTCGCGTCTGTCGGCTCGCGCACGTGGTCTGTCACCAGTCAACGTTAACGCC
GCCGCACATGTCCTGCGGCCGGGCAAAACGTGAAAACGAGCGGGCGACTGCAATGTCATGACACCGACGCGCGCGA
TGGGCCAGGGTCTGGCAGATTGATCTGTGCGGCCAGTGCCAGCAGCGTCGCTCGTATACGGCCGGCCGACGAGT
TGAACCGACATGGGCATGCCGTGCGCGTCGAAGTCCACGGCACACGGCCGCGGGTGGCCGGTCAGATTCCANACT
TGAAAGTACTGAAGCCGCTGCACCACAG (SEQ ID NO. 242)

Clone Rv231

.....Rv231SP6.seq.....
CGAAAGCGTGAAACAGCTCGCGGCAGCCCCGACGTGCTGCGTCCGATAGCCGGCGGGCGAAGATCAATTCCAGGCAG
CTCCCGGACAATGCGGCTCTGCTGGCCCGCAACGAAGACTCGAGGTCAACCCGGTGCCCGGGGTCTGGTGCACCTG
CCGATCGCACAGGTTGGCCACAACCGGCCGCTTGATGCCCGGTCCGCAAGCCCGGAGTTGCCAAACCCAGCGTGAT
CNTGCTCNGCTCTNTANTTCGGCGAAGAAGTGGCTCGCCTGATCACCTACCATCGGCCAGGATCTGCGTGTCATCACA
ACGCTCGCCAAGGAGGTTGTTGTG (SEQ ID NO. 243)

.....Rv231T7.seq.....
TCCGCCACGCTTCGCGCCGCCCGCATACGGCGCGTACCGATCTCCGCGTCATACACCGCGGGTAATCGCCGACGGTG
CCGGTTCGCGAGCCGAAGGTGACGACGCTGATTGAATCGAGTTCAGGTCCAGCGGGTGGCGCAGCAACGGCGGAGC
TCAACGACGTCAATCAGTTGTGCTTTCTACGGTCACCGACCCGGTGACCGTAGTCGCCCCGGTGCCTCGGCCGAGA
AGCTGCACCGCCACCGCGACACCGTCTTGACGCGGACCCACCCCGGATCGGTTGTTGGCCAAGGTAATTGGGTC
ATTCCATTGACGGGACGCCGACCC (SEQ ID NO. 244)

Clone Rv232

:::Rv232SP6.seq:::

CATTCTTTAACAGTTGTTTTGGGCTCGGCATGGTTAGCCAACGTTCTGCGGTCCACCATATCATCTTGGTCCGGTAGC
GCTCGTCCGGGTATGCTGCCGCCGGGATTCTCGTGTCTATTACTCCCCCGAAGAACC GCCACCGGTCCAGCGCGTG
GGCCGNCGCGGTCCCATCACAACTGAACCCCAACAGGGACATGCTTATCGGTAGGGCGCGGCCAAGGCGGCAGCA
ATCGCATCACTGCGCTCTGCGCGTCACTATTAAACCCACCCGGACTTCAC'TCCACCACCCCGAATGGCGCCCGGT CAT
TGATCATCTGGCGCACCGCGGATAA (SEQ ID NO. 245)

:::Rv232T7.seq:::

CGGTGTCTGCAGTTGGTAGGCCTGCAGTTTGTGCATCATGCCGATGCCGCGGCCTCGTGGCCACGCATGTACAGCAC
CACGCCGCGCCCTCACGGGCGAACATCGCCAGCGCGGCGTCCAGCTGAAGCCCGCAATCGCAGCGGCGTGACCAAAC
ACATCGCCGGTCAAGCACTCCGAATGCACCGGACAGCACGTCGTCACCGTCGGCGTTGGGCGCGGCGATCTCGCCGC
GGACCATGCGCGACATGTTCCACGTCCTCGTANATGCTGGTGTAGCCGATGGCGCGAACTCCCATGACGAGTCGGA
ATCCGCGCCTCGGCGACCCGCTCAATGTGCT (SEQ ID NO. 246)

Clone Rv233

:::Rv233SP6.seq:::

CGGCATCTGGCGGCTGAACCTGTTCTTGGGCAACATGCCGAGGATCGCCTCTTCCACCACGCGGTGGGGTGGCGTTG
CATTACCTCACCGATGGTGCGCTTGTGCAGGCCCGGGATACCCGAGTGCCGGTAAACCATCTTGTGCTGCAGTTT
GTCGCCGCTGATGGCGACCTTGTGCGCGTTGATCAGGATNACNAATCACCGCCANCGACATTGGGGGCGAACGTCGGC
TCGTGCTTGCCGCGCAGCAGGCTGGCCGCCGCGACGCAAGGCGCCAACCACACGTCGCTGGCGTCGATGACGTACCA
CCATCGCGTGGTGTACCCGCTTGGGC (SEQ ID NO. 247)

:::Rv233T7.seq:::

GCGGCAAAAATTGAAGCACTCNTGGCCACTNCCGCCGGAGGGACAATCTCGGGCGGCTAGGGCTTCTCGCGGGAAGG
CCCGAACGTAAGCTTCAACACGTCGCGTCGCCCTCCGACCGCAACATTCTGGGATGGCAGCAACCTGTAGCAC
CCTGGCCGGGCGATGATCTGCAGCGTCGCCGCGGGTAGTCGCCCCGGGCGGCTACAGTCTGAAACGCGATGACCATC
GATGTGTGGACGCCGCATCCGACNCAACGGTTCCTACACTGTGATATGTTGCGCTCGCTGCGCCGGTGGACGGTGGGT
CTATCCCGGA (SEQ ID NO. 248)

Clone Rv234

:::Rv234SP6.seq:::

CGCGTTGAAGTGAAGGGGTGCCGCCCGGCTCGAGCAGGCAAGCCATTTGTTGATGCGGTTACCGAAGATCTCTTCGG
TGAAGTGCCTGCCGCCCGGCCAGCTCGGCTCAGTGTCCGGCGTTGGTTCGCCGCGGCGACAATCTTGGCGTCCACGGTGGT
CGGGGTGATGCCCGCGAGCAGGATTGGCGAGCGGNCGGTCAGCCGGGTGAACTTCGTCAAGAGCTGACGCTGCGGTTG
GGGAGGCGAATCATGGTGGTGCCTGAGCTGAGTGGCCCGG (SEQ ID NO. 249)

:::Rv234T7.seq:::

TGACAACGCGGCGCGGATTACCCCGCTACCGCAGCAGCATGACGCGGTAGCGAACACCGCCGGATGCAGCGCAGGTGC
GTCGATGTGCTCACGGAATCGCCCCGGCACCGCATCTCGAGGATCACCAGTGCCACCCCTGCAGCGCGACACCGAC
GATTCGCTACACCGCCACGCCGATCAGGCCCTGGGCCAGCTGATTGGAGCTGGCGTATATGGCGGCGATGGTGACGAT
GGTCATCGCCTTTACATTGTGGCGGCCAGAACCGCGTTGGGGCGGCGGTGATGAACACTAGGCGACCANATCC
CCGGGTCAACAGGTTGACCATCC (SEQ ID NO. 250)

Clone Rv235

:::Rv235SP6.seq:::

CGCGGACATCCCGAACGAGGACACGCGACCGCTTCGGTGTGTGATCTATCAGGGCTCGCACCACGCGCAACCGCTTCC
GGCTACCTAGACGCGGT (SEQ ID NO. 251)

:::Rv235T7.seq:::

GCATGCGGGTGATGCCGTTCTCAGTGCGCAACAGCGTTCGACGCGGCATACCCAGCCGCACATGCCGTGCACGCCGNG
GCCGGGGCGGGAATCT (SEQ ID NO. 252)

Clone Rv237

:::Rv237SP6.seq:::

CTCAAGCTTCAGNCCNTCTAAGCGGTCTGCGCGGCGATCGCAAAGATCGCCCTTTGCCGGCGTTGGGGGCTTCTGCTC
GGGGGTGTTGTACACCTTCTCGAACACCTCGGCACCGACACCACCGCTCGGCTTGAACACCGCCAACATCGGCAGC

ANATCTTGATGTCCTGGTGAATCCACGGTGACTTTGGAGTGGAAGGCGGCCATACTGATCGCGCGCGCCACCACATGA
GCTAGCGGCAGGAAAACAGCAGCCGCTCACCTTGCGCAGCAGCGTCGGGTGATATGCCTGGCGCCC

::::::::::Rv237T7.seq::::::::::

(SEQ ID NO. 253)

AGTCGAANGTCAGTCCGGTCTCCTCTCCGACTACGGCCAAGAACTGGGGCGACGGGTGTGAGTGCAGAACAGCGGAAAC
TGGTGGCGCCTAGGCGAGCGAACGCTCACAAACGGCGGTGACCGCTTCTGGTGTGACCATCGAGCCGTGCCAGC
CCGGCCGCGTGCCGTGAGCCGCATCCACTGGATGCCCTTCTCGGCGGTTTCAATCANGTACAGCGACGTTCCGCCACC
ATCGTGCCGGGGCAGGTTAGCGAGAAACGCCGACTTCACCGATTGCCTCGGTGATGxxxxx (SEQ ID NO. 254)

Clone Rv23

::::::::::Rv23T7.seq::::::::::

AGCTTCGCGGCGTGGCGATCGCGGTTCAAGGCGCGCTCTTCGAGCACAACGAGCGAAGACAGCTCGGCGACGGAGCCT
TTATCGACATCCGTTCCGGCTGGCTGACCGGCGGCGAAGAACTGCTGGACGCGTTGTTGTGACGGTGCCGTGGCGAG
CCGAGCGCGCTCAGATGTNCGACCGGGTGGTTCGATGTGCCGCGGCTGGTGAGTTTTACGACCTGACCATCGAAGATC
CGCCGATCCGACGCTGGCGCGGATGCGCCGGCGGCTCAACGACATCTACGGCGGCGAACTGGGTGAGCCCTTACCA
CCGCGGGGCTGTGCTACTACCGCGACGGCTCTGACAGCGTCGCCTGGCATGGCGACACCATTGGTTCGCGGCAGCACTG
AGGACACTATGGTGGCGATCGTCAGCCTCGGCGCCACCCGCGTCTTCGCGCTGCGGCCGCGTGG (SEQ ID NO. 255)

Clone Rv240

::::::::::Rv240SP6.seq::::::::::

AGCTTCAGCTGATACTCGACCAGCCCCACTCGGGCCAATACGTGAATGTCTAGCATCTTCACCCGTTACGCGGCTANT
CGAGTAGTAGACATTGATTAGCCTGAACGTACCTCCGACGCCAGCTGACGAACGGGTATGACGGATGGATTTCTGGT
GTGCGGCCCGAGGTCAATTCTTACGGATGTATCTCGGGGCCGATCGGGGCCGATGTTGGCGGCCGCGCGGCCCTGG
GACGGACTATCCGACGAACGGCGGTGGCGGCGTCTGGTTTGGGTGGGTGACCTCGGGCCTGGCGGATGCGGCGTGG
CGCGGCCCGCGGCGGTTGCGATGGCNCGCGCGGT (SEQ ID NO. 256)

::::::::::Rv240T7.seq::::::::::

CTGGTCATGGACGTTGCTCCGGTAGTGGCTCACTGCCGATCCTCCTCGTTGAGAGTGCCACCTCAGGGTTGGGTAGGG
TTGGGTACTCGAAACCAAGTTACCCACCAAGTAACACCGTCAAATATATCCGTTGCATAGGTCAATGCAAGTTGATGT
GAGCTACATTGCACCAACTAACTAACCAACCGGTTGGGTAGCGGTGATCCTGGCCGTGTGGTCTCTACCTGCGG
TGATAGCGATCAAATGAAGAATATGCGGAGTCTAGGGCGGCAGCGCCTGGCANCGTAGATCATCGGCTCACGCGGATG
CGGCCTCTTGGTACGGACATGCGCGCG (SEQ ID NO. 257)

Clone Rv241

::::::::::Rv241SP6.seq::::::::::

CTCGTAGTAGCACCCCTGTAATTTGGGATCGGCAAAAAGGCGAATCACCGCGTGGCCACGACACGCCGGGAGGGACN
ATCTCGGGCGGCTAGGGCTTCTCGCGGGAAGGCCCGAACGTACGGCGTTTCAACACGTGCGCTCGCCCTCCGACCGCG
AACATTCGGGGATGGCAGCAACCTGG (SEQ ID NO. 258)

::::::::::Rv241T7.seq::::::::::

GGATCAACTACCGGCCAACGGTGATTCTTGGGCGCCGCTGACGCGCGAAGCAGCCAGCGACACATTGAGCAGATGGCC
AGCGGTGCCGGGCCACGATGTTGGTGCTCGGCGGCTACTCCCATGGTGGGCNCGTGATGACATCGTCACCGCCCG
ACCACTGCCGGCCTCGGGTTCACGCAGCCGTTGCCGCCCGCAGCGGACGATCACATC (SEQ ID NO. 259)

Clone Rv243

::::::::::Rv243SP6.seq::::::::::

AGGACCGTCAGCACGGCGACGTGCTACTCGCCGAGCAGTGGGAATCGCTCTGCAGCAAACCACTTACTCTGCGCGACGT
TCGAGATGACCTTCTGAATGGACGGATCTACCTGCCGCGCAGCAGCTGGACCGCGTATGCGTCCGCCCTCCGCCTGGA
CGACACCGGGGCACTCTATGACCCCGACGGACGGCTCGCGGTACTGCTGCGGTTACCGCCGACGCCCGCACGGTACG
CGTCGGGACTGCGCTGAGTCCANCCTCGACGCCGTAGCGCTGCTGCTGTGCGGCCATGTCTGGCATCTACCGCCGTCG
CTCCCTTGA (SEQ ID NO. 260)

::::::::::Rv243T7.seq::::::::::

CGACTCTGTTGGCCACTGCGGGTTCGATCTTGCGGCCGCCCGGTCGTGGAACGCCAGGTACCCGGCGGGCGCACCGC
GGTCAGCGCGTCTGTTGGCCAGCGTGGTCACATGGAAGTGGTCGACGACGAGCTTGGCGTTGGGCAGCAGCCCGGGCGT
GCGGATCGCCGAGGCGTATGACGCGCGGGGTCGATGCGCCACCGTACTGGATGCTCTCCCGGAAGTGGGTGTGCGCG
CTTGACGCCATGCCAGCACCGCGCGCGCGCGGCGCTTCATGCTGCCCATAAACCTGATACCGGCCAGGTTCGACNA
ACNGTATCCACGGTCAACCC (SEQ ID NO. 261)

Clone Rv244

.....:Rv244SP6.seq:.....:
CACACGGACGGCGGTGCGGACGCAGCTGACGCGCATGGTGGTCAGCATCGCGGCCGGTCTGCTGTTGTATGCCTACTT
CGCGCCGCGCAAATGCTGGTGGGCGGCGGTGGTGGCGCTCGCATGGCTGGGCTGGGTGCTGACCCAACTCTCGAACCA
CACCGGTGGGTGGGCTGGGCTATGGCCTGCCATATCGGCCTGGTGTCTACN (SEQ ID NO. 262)

.....:Rv244T7.seq:.....:
CCGATATCCGAGCCGATAGCTGGCGGGCTCGGGTGGTNGCCAGCGGCGCTGCGACGAAAGTGTGACCGTCATGAAACA
GACACCACGGCGGCCGTGCGCCGTGCTCACCTGCTCGAGATCTCAGCATCCGCGAGCCGGTGTGATCGCGCTTTTCGGC
GTGTAGTGGGTGCGCGCCCGAGCCCGGCAAACGCCGGCCCGACACAACCCCGGAACAGGAAGTCCGGTCACCGCGCC
(SEQ ID NO. 263)

Clone Rv245

.....:Rv245SP6.seq:.....:
GCTTCAGGACAAATTGNATCCCTATGCACCCGTTGTCACGCCGATGAGTGAAGACTGCACGCAATCGCCGGAATCCGG
CAAAACCCTGCACAAGCGAAATCAACCGGAGGCTGACAAGGCAACGTCGGTGATCCGTACCGCCTGGTTGGACAAACG
GCAGAAGGCGCCTCGTCCGGTCCATCTACGCCGAGCACACTGGTGATAGCGCCATCGGCATCGGTGCGGCCACGGTGG
AGACGAACGTCCGCNGGCGTCTGGGTGAGTAACCCGCCGACCAAGTCTCGGGCAAGCTGGTCAACATCGGCGCCACG
TCTCCAAC (SEQ ID NO. 264)

.....:Rv245T7.seq:.....:
GTTTGGCGCCTTATTGCACTGAGGTGCTCAATTGACCCACAGCGGAAATGCCGACTATTGCGAGGCCTCCTTCGCCT
TGGCTGCCGGAGATGGGCTCCGCGGGAACCGCATGCAGGTATATGACCTCGGTTTCTCGGGTGCTACCGCGTGCCTTG
TCGAGGATGAACTCGGCGTTGGAATTGTCCAGCCGGCCCAATTCATCGAGCGCAGATTTCGTACACATGGCCGGCGGCG
ACATACCTTACCGTGGATCTGCTCCACACGGACCGCCCTGTGCGGATCTGCTCACGGGTAAAGGAATTA
(SEQ ID NO. 265)

Clone Rv246

.....:Rv246SP6.seq:.....:
GCGCACTCCTCCTTATCGCTCCGCTCTGCATCGTCGCGGCGCGGTGTCAGGTGCAAACGCCTTCGGGGGTGGGGGTCTTG
CGGAGCACACCGGATACGGAGCGCAACGCGTCGCGTTGTGCGGGCAAACAAGTGTGCAGGNCCATGCCATGTCCAG
CAGCTTATCAGTGTGGAACGTGCGAACGTGCGCCTTCGCGGTGCTGAATCTCTACAAG (SEQ ID NO. 266)

.....:Rv246T7.seq:.....:
CGCTGAAAGCCACCATTCGCGGGTCGGGCGCCGGGCTCGGGCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCG
CGACACCACCGGCTGCGCTACGTGAGCCATACCGGGCGGAGCTACATCGGCTCGGCCGCCTAGTGTTCGGGNCCTC
TTTCGAGGTGAGGTGCA (SEQ ID NO. 267)

Clone Rv247

.....:Rv247SP6.seq:.....:
TGTAATTTGGGATGGGCAAAAGCAAANCACCGGTGGCCACAAACGCGGGGAGGGACAATCTCGGGCGGCTAGGGCT
TCTCGCGGAAGCCGAAACGTACGGCGTTTCAACACGTGCGCTCGCCTCCGACGCGAAATTCGGG (SEQ ID NO. 268)

.....:Rv247T7.seq:.....:
CTTGGGCAACATGCTGAGGATCGCCTTTTCACCACGCGGTGCGGGTGGCGTTGCATTAGCTACCGATGGTGCGCTTG
TTGCAGGCCGCCGGGATACCCGAGTGCCGGTAAACCATCTTGTGCTGCAGTTTGTCCGCTGATGGCGACCTTGTGCG
GTTGATCACGATGACGAAGTCACCGCCATCGACATTGGGGGCGAACTCGGCTTGTGCTTG (SEQ ID NO. 269)

Clone Rv249

.....:Rv249SP6.seq:.....:
GCATGCTTCATTATCTAATCTCCAGCCGTGGTTTAATCAGACGATCGAAAATTTCATGCAGACGGTCCCAAATAGAAAG
ACATTCTCCAGGCACCAAGTTGAAGAGGTTGATCAATGGTCTGTTCAAAAACAAGTTCTCATCCGGATTGAACTTTACC
AACTTCATCCGTTTCATGTACAACATTTTGTAGAACATGCTTC (SEQ ID NO. 270)

Clone Rv24

.....:Rv24SP6.seq:.....:
ATACTCAAGCTTGATGCCGCCGAAACCGAGCGTGAGCACGCCGCCAGCCACCACGCGCGGGTGGGGCGCCGGGCCCGG
GCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCGCGACACCACCGGCTGCGCTACGTCTATCCATACCGGGCG
GAGCTACATCGGCTCGGCCGCCCATTTGTTNCGCCCTCTTTTCAGGTCGAGGTCTATACCGATTGCGCATCCG
(SEQ ID NO. 271)

.....Rv24T7.seq:.....
TCCGTACTGGTCGGGTACGCTTCGGTCGCAGTGTGCGAGTGATAGATGACGACCGGGACCTCGTCGGCATCTTCCATA
GCCCCGCACACCTTCAGTTGCTCACCAGGAATCCAACCGGTAGAAGTTCGGCGAGCGCTCGGCATTGGTCATCGGGATA
TGCCGCTCGGGACGGTCAGAACCTCGGGTCCG (SEQ ID NO. 272)

Clone Rv251

.....Rv251SP6.seq:.....
GTTCTCGCACGATTTTCGGATTAGCGGGATGGTCTCAATTGGGTATGCGGGGAAGGCGCTGACATTCGCCGCGATTAGC
TGTTTGATGGACCGGGGGTATTTTGTATCACGGAAATGGGTGTTTATNCAGGTCGCACGCTTTCATCCGGGGCGGAA
CG (SEQ ID NO. 273)

.....Rv251T7.seq:.....
GGGTGTGCTGCTGTGTATGCACGGCATAACGGACATCCTTCCCCTGAAGACCGCGGTGGAACAGCCACGTGTCCATC
ATCANGGGGTCAACCCCGGCCAAGGGCGACGGCAGCCAAAGTTCGCCGACCGTTAACCTAGTGCTGTAGCTTCATT
GCTGCGAGCAAAACAGCTGGTCGGNCGTTAGGAATGAATTGAACTCAACCGATTGGTGCCGCCGTAGGTGTCTCTG
CTG (SEQ ID NO. 274)

Clone Rv252

.....Rv252T7.seq:.....
ACTACCGGCCAACGGTGATNTCTTGGCCGCCGCTGACNGCGCGAACGACGCCAGCGACCACATTCAGCAGATGGCCA
GCGCGTGCCGGGCACGANGTTGGTGCTCGGCGGCTACTCCCANGGTGCGGNCGTGATCGACATCNTCACCGCCGCAC
CACTGCCCCGGCTCGGGTTACACAGCCGTTGCCGCCCGCAGCGGACGATCACATCGCTTTTATTNNTNTTCNGGAAT
CCCTCGGGCCCGCTGGCGGGCTGATGA (SEQ ID NO. 275)

Clone Rv253

.....Rv253SP6.seq:.....
ACGTCGGGANACTGTTTCGCGTTCATCCTCGTCTCGGCGGATTGGTCTGCTGCGCCGGACCGACCGATCTTCAGCGGGG
GGTCACGCTCCGTGGGGTGCCGTTACTTCCGATCGCCAGTGTGCGCGTGCTGTGGCTGATGCTGAACCTCACCGCGT
TGANTTGATCGGTTCCGGATCTGGCTGGTGGCCGAACGCNATTTATGTCGCTACGGGCGCCGGC (SEQ ID NO. 276)

.....Rv253T7.seq:.....
GCTCAAAGGCACTACTGGCACCAAGGCCACACGTACCTGTGACTCCTGCGCCGACCCGCCGAGGTCTGGCCGTTA
CACCGAACGGGCGAGCCGGGAGTTGGTACCATCGAACAAGACAAGGTGCATGGGCGGAGTTGTTCCGCCACTTCGTCG
ATGACGGGTC (SEQ ID NO. 277)

Clone Rv254

.....Rv254SP6.seq:.....
CGATACCGGCTGCTTACCGAGACATCCACCATGCCACCCGAATCACCGCACGCGCCGAAATCGCACAACAGCTTGACG
CCTTGACAGGTTCCGCGATTGGAATTGCCGACGGTCTCTGACGGCGTCGACCTTGGCAGCCTCTACGAGCTCTCGGAAT
CACTTGCCACAGCGGGGTTTCGATGAGTGTACACCGAAGACCTCGATATGGGCGCAATCCTGGCCGACACATCCAAC
CGGGTGTTGTGTGCTGCGGCGCCGGTGGGGTCNGCAANACACTACCGCGGCGCGCTGGCGTTGCGCGCGGCCGAAT
ATGGCCGCACTGTGGTCG (SEQ ID NO. 278)

.....Rv254T7.seq:.....
CGTCGTCGTCGTGGTATGCGATAGCCATCCCGTCGGGCTACTCGCCATCACCGATCAGCTTCGCCCCGAAGCCGCCGC
GGCGATTTCCGCTGCGACCAAACCTGACCGGGGCCAAACCGGTATTGCTTACCGGCGACAACCGGGCCACCGCCGATCG
GCTCGGTGTACANGTTGGCATCGACGACGTACGGGCCGGGCTACTGCCGACGACAANGTCGACGCCGTGCNGCNGCTG
CAAGCTGGAGGTGCCAGATTGACCGTGGTGGTGACGGTATCAACGACCTCCGGCCTTAGCGGCCGCGCATGTCGCAT
CGCCATGGGCGAGCCCCGAC (SEQ ID NO. 279)

Clone Rv255

.....Rv255SP6.seq:.....
GCACGCAATCGAAGTCACCCAAACCGGGCGGGCCAGGCGTCTNACGCCACGTNACCAGCCGCAACCTCAACCCGGCC
ACGGCGAGCTCCTGATCAAGGCCGAGGCCATCGGTGTCTACTTCATCGACACCTACTTCCGCTCCGGGCAATATCCGC
CGCAACTCCCGTTCGTTCATCTGCTCCGAAGTATGCGGCACGGTGGANGCCGTCCGGCCAGGGGTTAC

(SEQ ID NO. 280)

::::::::::Rv255T7.seq::::::::::
TCGACTGTGTGGCCACAGATCACGCCCCGCATGCCGAGCACGAGAAATGCGTCTGAATTCGCCGCGGGCCGGCCGGCAT
GCTCGGGTTGCAGACGGCATTGTCGGTGGTGGTGCATACAATGGTGGCGCCGGCTTGTTGANTTNGGCGCGATATCGC
GCGGGTGATGAGTGANAACCGCGTGCA (SEQ ID NO. 281)

Clone Rv257

::::::::::Rv257SP6.seq::::::::::
GAACCTGACACCCTGGTCACGGGTGAGCACGGACTTGATTTCTTCNCTATTGGTCGGCGCTGTTGAGCACACCACGCC
GCTGACGGCCGTCGCGTCTCGCTGTGCTCGGTCTGGTGGAGCGCGCTGCCCGGGCCNAACATCNTAAATCAAGCGT
ATTCGTCAACAGATATCATCAATGTCGGCGCTGGACTATTCAAATCATCGATATACTGGTGACCTGGTCTTCGCCAT
CGATCAATGGCGATAGTCACGCAAATCGTCACGGACATCGTCGGCGTCCCAGCTGGCCCGTCCCAACAGATGCTGCAA
CCCATCGGGGTGGTATCACCGCGGTGCTCGGCGATGGTCCACAATTCTTGCGGTCCAAGCCCNAAACATCCCGGGCAT
GAATTCACCGGCATGCGCN (SEQ ID NO. 282)

::::::::::Rv257T7.seq::::::::::
CTATCGTACCCGCGCCGGTCACCTTCTGGATATCGCCGGCCTGGTCAAGGGGGCGTCCGAGGGAGCCGGGCTGGGTNA
CAAGTTCCTGGCTCATATCCGCGAATGCGACGCCATTTGTGAGGTGGTGGGGGTGTTCTGTCGACGACGACGTGACTCA
TGTACCCGGACGGGTGATCCCCAGTCCGACATTGAGGTGTCGAGACCGAGCTGATCCTGGCAGATCTGCAAAACCT
GGAGCGGGCCACGGGCGCGCTGGAGAATGAAGCGCGCACCAACAAGGCGCGCAAGCCGGTCTACGAAGCGGCACTGCG
TGCCAGCANGTGCTCGACGCCGGGCAAGACGCTGTTGCGCGGGGGTGGATGCCGCCGCTTGCGCGACTGAAACT
GCTGACCACCAAGCCCTTCCTGT (SEQ ID NO. 283)

Clone Rv258

::::::::::Rv258SP6.seq::::::::::
TACTCAAGCTTCAGGCCGCCACGTCCGCCGTCCGTGCGCGACGTGACCTCGAGCGCCGAGTTCGACTCGACATCGCCG
CCGGCGCATGCCGACATGAACGCGGCACTCACCGCAAGCCCGTCGGACGTGAGTTCGATCGACTCCGCTTCAAGCACC
GGATCGTCCGGGCACTCGCGGCCCTCGGCCTGTGCGAACGGCACACCCGTCGTGGCGGCNCCCCGCGCGGAAGTGGG
TCATCACGGTCGTTGCGAGCCGGTCGCGTCACCGCGTACCGACGCCGTC (SEQ ID NO. 284)

::::::::::Rv258T7.seq::::::::::
CCGACATCGAGTGGGCTCGCAGTGACTTGCGGACCTCCAAGCCACCGGTACCCGCCGCGCGGCAAGCCAAGGACGACG
ACGGCCTTGCCGATAGCTGCGCCAGGCGTTGCGCCAACTGGCGTCCAGCGTCGCCACGATCGTCAAAGAGCTTCATC
TGCCGAGTGTGTCGCCATCTCATGGCTCCAAATATGGAATTAGGTCCCTGGGCGACTGACGACAGTCCCTCAGCGAC
CGGATTGCGCATCCCGCCTTGACGCTACTCCGCAAATCCCGGGCTTGCGTCCGCGGAAGCGAACTCGGCGGGCGCTAC
GTGGTGGTTCACTTCGGCCGTGCGCACTCGGATCGACGGGCGGATGGTGGCCGGGCGCGCGCTTCTTGGTCATCCG
ATTGAGT (SEQ ID NO. 285)

Clone Rv259

::::::::::Rv259SP6.seq::::::::::
ATACTCAAGCTTGTGCGGTAAACCGCACGCAGGGCGGTGGGTGCGGTGTCAAAGACACCCACACTTCTTTGCGGTTT
GGTGATCTCGACACCGGCGGAGCCGACCACTGCGCGCTAGATCGGCGATCAGCGCGTCGGCTATCGCCTGGGT
GCCGCCACCGGAATCGGCCAGCCGACCGAATGGGCCAGCGTTGCCAGCATCAGTCCGGCGCCGCGACACCACTGA
CGGCAACGGTGAAATCGCGTGGGCGGCAACGCCGTTGAACAACGCGCGGCATCCTCGCCCGCCAACGACCGCCAGGC
AGGGTGCCTGGGCCATCATCCGAGCCGA (SEQ ID NO. 286)

::::::::::Rv259T7.seq::::::::::
TGGACTCATAACGATCGGGTCAGCGACGCGCCAACACGAACGGCCGGACGAGTGGGCCAGGGTCGCGCCTCCCCTACA
AACAGGATCCGTTGCTGCGAGCGACAGGCTCCGGTGGCGGCTTGGGCGCGTGCTCGTCCAGCGTCGGGTCCCGGG
TCGCGGCGGACGCTTGTTCCTCATACTCGCCCCCTAATCTCGAGGCGAGCCGTAACCGCAGGCAACCTCCCAAAA
TGCAATCCCCCAAATGCAATGCGTCGAGCTATTCTCACACCGACCGTAGTTGCGGATCAGAAATCCGTTGGGCGC
GGAAGTCCAGCCGAATTTGTTCTCCCGCTCCGCATCATGCTTGTAATCGTTTGAAATCATCTCATATGCCTCGATC
GTTTCATAGGTCAAGCCCAAACCCGGCAGGATGGGTGGCC (SEQ ID NO. 287)

Clone Rv25

::::::::::Rv25SP6.seq::::::::::
CTTTACACTTTATGCTTCCGGCTCGTATGTTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATG
ACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTAGTGGTTGCGCACGTAAATTCGTGAGT
GACCGATCCCCTGCTGTCTCACTCGCCTCACAGCGACCAACACGGCTGGCGCTCAAGGCGGGCAGTGGCGGAGCAGAT

GAGGAATGTGCGACGTCTTGATGCAGCCTGTCAGAACACCGAGACCCTCGACGAACTTACGATCGAAACCGCTTAGGC
CAACCGGTGACGGGGGTGTCTTCCGCGGCTAGGGCGCCTTATCGTCCGAAGGCCGTGGGTGGTGATCGCCTTCTGGG
TCGCGCTTGGGGTCTGCTTGGCCGACGGTGCCGTCCCTGGACCGATCTCCAGCGGCATCCAGTGGCGATTCTGCC
ATCGG (SEQ ID NO. 288)

.....Rv25T7.seq:.....
CAGGCATGCAAGCTTGCGATGTATCAACACGCCGTTGCGCAGCGTGAGCCGATAGTTGACATCCGGCTCGGTGAAGGT
GAAATCGATGGCCAGGTGAGGTCCCATGCGCGTGGGCCATTGATGCTGATCGCCAGGACGTCAAAGATTGGTCCGG
CGTCAGCTGGGCGAAAAACGTGGGCGCCGGGACTTGCCCGGAGCTGCCCGGGTTCCTGCGCAGCTCGGCGGCCCC
GGTCAGAAAGAAATTGCGCCAGGTGCGCACTCCGCGCCGTAGGCCAGCTGCTCCACGGTGTGCGCATATAGCCCGCG
GGCCGACGCTGCTGCTGTCGGCGAACACCGCATGGTCGAGAAGCGTTGCCGCCAACGGAAATCACTGCGTCAAAG
CTTCGCCGGGCCACTCCAGCACTCCGTC (SEQ ID NO. 289)

Clone Rv260

.....Rv260SP6.seq:.....
ATACTCAAGCTTGACCGACGCTGATCGCACCGCACGGGAACCTCAAGGGCACTACTGGCACAAGGGCCACACGTC
AACCTGTAACTCCTGCGCCGACCCCGCCGAAGTCCTTGGCGTTAACACCGAACGGGCCAACCCGGGAATTTGGGT
CCATCAAAACAAATAGCAGGTGCCTGGGCGAGTGTTT (SEQ ID NO. 290)

.....Rv260T7.seq:.....
GTCGTGCTGTGCTGGGCGTCCGTATCAGCACGCCACGAAATGGGGCACAGAAGGATTCTGGAACGGTGGCTGTC
CAAGATCACCTCGCCCAAACTGCTACGGGCACTTCTACATCGAGCACAAACCGTGGCCATCACGTCCGCGGTGTCCA
CACCGGGAGG (SEQ ID NO. 291)

Clone Rv261

.....Rv261SP6w.seq:.....
ATATGCCTTGCTGAGCTTTTCGGATCGCAGCGAGTCGTACCCGCGCCGGTCACTTCGTGGATATCGCCGGCCTGGTC
AAGGGGGCGTCCGAGGGAGCCGGGCTGGGTAACAAGTTCTTGGCTCATATCCGCGAATGCGACGCCATTTGTCAGGTG
GTGCGGGTGTTCGTGCAACACGCTGACTCATGTACCGGACGGGTGATCCCCAGTCCGACATTGAGGTGCTCGAG
ACCGAGCTGATCCTGGCAGATCTGCAAGCCCTGGAGCGGGCCACGGGGCGGCTNGAA (SEQ ID NO. 292)

.....Rv261T7.seq:.....
GACACCCTGGTCACGGGTGAGCAGGACTCGATTCTTCGCTATTGGTTCGGCGCTGTTGAGGCACAGCACGCCGCTGAG
GCCGTGCGTCTCGCTGTGCTCGGTCTGGTGGAGCGCGCTGCCCGCGGCCGAACATCGTAAATCAAGCGTATTCTGTC
AACAGATATCATCAATGTCGGCGCTGGACTATTCAAATCATCGATATACTGGTGACCTGGTCTTCGCCATCGATCAA
TGGCGATAGTCACGCAGATCGTCACGGACATCGTTCGCTCCAGCTGGCCCGTGCCAAACAGATGCTGCAACCCATCG
GGGTGGTATCNCGCGGTGCTCGGCGATGGTCCAACAATTCTTGGCGTCCAAGCCCGAAACCATCCGGCCATGAGTTC
ACCGGCATGGCGCAACGGCTGGTGCAGGGCAAACGCGGCGCGATCGAATTC (SEQ ID NO. 293)

Clone Rv262

.....Rv262SP6.seq:.....
TGTAAGGTTGGTCCCGTCCAATTCGCGGCGGGCGCGATATGCCTTGCTGGTCTTGCTCATTTGATATCCAATC
TATGGGTGCTGGTTACTCAACGGGCCGAAGCTGGCCCTCCACGGGTAGGGTCTATTTCGACGGTGATGTCC
(SEQ ID NO. 294)

.....Rv262T7.seq:.....
CCCGAATCCGGTGGCCGGCAGGGGGCTGGCGACGTGGACACCTTCTAACTTGTCTTTACCGGTCACTGTTGCACCCC
AACACCTTTAACGACGTGGACGGACGTACATCGGATTCGACGGTGTATCCACAGCGTTGCCATTGGGCACACCCAC
TACGCCAATTTCTCCGACTGGGACCTACCGCAGCCTCGCCCCACTGCAGGGACTGTTGTTCCCGCAACGGGCCATC
GACATGATCCAGTCTGGTGACCGACGCGGAGCAGACTGGTGCGTATCCGCGTTGGGCGCTGGCGAAATTCGCCAC
CGGCATGAT (SEQ ID NO. 295)

Clone Rv263

.....Rv263SP6.seq:.....
TTGAGATGCTGGTCGGGATGCCGATGGTTGGAACATGGTCCCCTGGCGTCGAATACGCGCGAGCGCATGAGCTCACCG
GTTCCGAACAACGTATCGAAGAACTCGCACTGCTGGCAGATGGTATCTCCGATGTGGTTGTAATTTGTATCCCAACTC
TAACTGTGCTATCGGATCTGCGTGAATA (SEQ ID NO. 296)

Table 3 : End-sequences of the polynucleotide inserts cloned in the named recombinant BAC vectors contained in the I-1945 *M. tuberculosis* H37Rv genomic DNA library.

RvXXXSP6 corresponds to the SP6 end-sequence of the clone RvXXX.

RvXXXT7 corresponds to the T7 end-sequence of the clone RvXXX.

RvXXXIS 1081 corresponds to a region located close to a copy of the IS1081 repetitive sequence (Insertion element).

The character « - » denotes an uncertain base residue.

Clone Rv101

.....Rv101SP6.seq.....
 AATACTCAAGCTTGGCCAGCCGTCGATGACAAGAAATATGTCCGCAAAAGACTCAGCGGCCGACTTTGCTCGCAGCTG
 GCGGTACCGCGCCACCGATTCTATGCCGTGGTCGCGGAAAAATGCCTCCCGAAATCGCACGGCCGACTCCAGTTCGGC
 GAGCATCCGCGATGCCAGCTGCGGCTGCGCCTGCCGGCCACGGCACCCACATGCGGCAGTTCGTCCACCTGGGCCAG
 CGCCCCGCGCCGAATTCAAACAATAGAACTGCACCCGGCCCGCATCGTGGGTAACAGCCAACGCCATGATCAGCGT
 CCGCAGCGCGGTTGACTTGCCCGTTTGGCGTGCACCTACGAACGCGACATTGCCTGCGGCCCCGACAAGTCGATCGT
 CGCGGCCACCCGTGACTGCTCTAACGGGCGATTGAAATTCCGAT (SEQ ID NO. 6)

.....Rv101T7.seq.....
 CCACCCGTGTAATTTGGGATGGGCAAAAAGGCGAAGCACCGCGTGGCCACGAACGCCGGGAGGGACAATCTCGGGCGG
 TTAGGGCTTCTCGCGGGAAGGCCCGAACGTACGGCGTTTCAACACCTCGCGTCGCCCTCCGACCGCGAACATTCTGGG
 ATGGCAGCAACCTGCTGGCACCCTGGCCGGGCGATGATCTGCAGCGTCGCCGCGGTAGTCGCCGCCCGGGCGGCTAC
 ACTCTGAAACGCGATGACCATCGATGTGTGGATGCAGCATCCCGACGCAACGGTTCCTACACCGCGATATGTTGCGCT
 CGCTGCCCCGGTGGACCGGT (SEQ ID NO. 7)

Clone Rv102

.....Rv102SP6.seq.....
 AATACTCAAGCTTTCCGCGGATACCGCCATGTGCGGCACATCCAGGACTTCTGGGGGATCCGCTGACAGCGGCGGG
 ATCCCAAAGTGCGGATGATCGGGCCGCCTACGTCGTGGTGACCTCGTCGGTAACAACGAAACCGAAGCGTATGACTC
 GGTCCACGCGGTGCGGCACATGGTGGACACCACCGCCACCGCACGGGTGAAGGCCTATGTACCGGTCCGGCAGC
 ACTCAATGCCGACAGGCCGAGGGCGGAGACAAAAGTATCGCTAAGGTACCGCGATCACCACATGGTGATCGCAGC
 AATGTTGCTAGTGATCTATCGCTCCGTAATTACCGCGGTTCT (SEQ ID NO. 8)

.....Rv102T7.seq.....
 GTGCCGTTCAACCCGAATTGGCTTTCCGCGCCATCGGTGAGGACGGCGTGCGGGTGCTCAACGACGACGTCGTCCGC
 GGGACACACCTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGGAACGC
 TTCCGCGCGGGCGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGACGGCATCGCCACCGGAGCG
 ACGGCCAAGGCGGCGTGCCAGGTGCGCCGGGCGCACGGTGCGGACAAGTGCTGCGGGTCCCGATCGGCCAGAC
 GACATCGTGGCGAGATTGCGCGGGTACGCCGATGAGGTGGT (SEQ ID NO. 9)

Clone Rv103

.....Rv103SP6.seq.....
 AATACTCAAGCTTTCCGCGGAAACGGACACATTGCGAATATTGATGACAAAATAAAAATCATTGATGGTTTGGTACAC
 CAGGCCGATCAAGCCTTCGCCGAGCCAAATTCGAATCAAGAGGCCCAAGCCGTACCAATCAGCCCGCAACGAGGGA
 TTCCGTATTATCAGCCAAAATAACTGCTCTCGGGTTACACCCAAACAGCGCAATATGGCGAAAAACGGTCGCCGTTG
 CACGACATTAAATGTCAGGTATTGTAGATTAAAAAGATACCCAC (SEQ ID NO. 10)

.....Rv103T7.seq.....
 TGCTCCCGAAACCTGGGGGTGTCCTGCTCTGTATGCACGGCATACGGACATCCTTCCCCTGAGACCCGCGGTGCAAC
 CAGCCACGTGTCCATCATAGNGGTCAACCCCGGCCAAGGGCGACGGCACGCCAAGTTTCGCCGACCGTTAACCTAGTG
 CTGTTAGCTTCAATTTGCTGCGATCAAAACAGCTGGTCGGCGTTAGGAACTGAATTGAACTCAACCGATTGGTGCC
 GCCGTAGGTGTCCTGGCTGCGGGTGCGCTGGTGTGTCGCGGTGTGGTAACGACGACAATGTGACCGGGGAGGTGCA
 ACCACTGGCCAGGCGTCGGCAAGGTGATTGCGGGGGGAAGAAGACACTCAAAGCCAGTGGGT (SEQ ID NO. 11)

Clone Rv104

.....:Rv104SP6.seq:.....
ATACTCAAGCTTTGCCGACGAGCGGGCGATGTTGATGACGGGAAACCCAGCGCACAACCGACGATTTTGGCGTAGCC
GGCGGACGTCTGCTCGATTCCGATCACGTGCGCGCTCGCATCGAGCATGGCGCCGGCGACGGCTAGCAGCGATCCGCC
GTCGTCGAGGAGCACGACACGAGCCGTACGCCCGGCCGTAAGCCGCGCCAGGATTCGGCGAAAAACCGTTCTACGTG
GCGGGTGTACTGGGTGTGCAATGATTCTGTTGGGGTGCCTAGGCGTCGCTGCAATCGTCGACATAGATGCCGTGCGGCCG
CATCGCTGCACAACCTCCGGGTGAGTGGAATAGCACTTGCCGATCACCGGACGTTGCGCGGATGAGGCCGAACCCGA
ATA (SEQ ID NO. 12)

.....:Rv104T7.seq:.....
TCCTATGTCCCTGCCGAGCANGTGATCGAACGCGGTGACAGATTTGTCTATCCTGGACCTGACGGTGAGGTGCAAGTT
TTCCAGGAATTCGGCAAAATCGGTAAGAGCCTGAAGAATTCCGTATCGCCGGACGAAATCTGCGACGCATACGGGGGC
ATATACGCTTCGGGTTTACGAGATGTCGATGGGGCCGCTGGAGGCTTCACGTCCATGGGCCACAAAGGATGTTGTCGG
CGCGTACCGTTTTCTGCAGCGGGTGTGGCGCTTGCTCG (SEQ ID NO. 13)

Clone Rv105

.....:Rv105SP6.seq:.....
ATACTCAAGCTTGATTCCGCCGAAACCGACCGTGAGCACCCCGCCAGCCACCACGCTCGGGTCGGGCGCCGGGCCCCG
GCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCCGACACCACCCGGCTGCGCTACGTCTAACCATTCAGGGC
GAGCTACATCAGCTCGGCCGCCAGTGTTGCGGGCCCTCTTTCCAGGTCGAAGTCTATACCGATATGCGCATCCGCAGC
CGCCACCCTGGAGAACAGAACGATGCCCTACTAATGCTTGTCTGGCGGGGCC (SEQ ID NO. 14)

.....:Rv105T7.seq:.....
GGTACGCTTCGGTCGCAGTCTGCGAGTGATGCATGACGACCGGGACCTCGTCGGCATCTTCCATAGCCGCCACACCT
TCAGTTGCTACCCGGAATCCAACCGGTAGAAGGTCGGCGAGCGCTCGGCATTGGTCATCGGGATATGCCGCTCGGGAC
GGTCAGAGCCCTCGGGTCCGGCCAGCACTCCGCAGGCTTCGTCGGGGTGGTCGCGACGCGCATGGGCCACCATGCGAT
TCACCAGGTCTGCGCGAATCACCAGCACGTAGACGGTTCTTTCTAAGCAACACCGAAGTTTCAGGACCGGAATGCT
CCGGGAACATGTCACGGTAGGTCGGTATTCCGGCTACCGGCTGA (SEQ ID NO. 15)

Clone Rv106

.....:Rv106SP6.seq:.....
GGCGTCAACGGTGTCGGAACCCGCTCAAGCAATTGGTAGGCCTGCAGTCTGTGAATCAGGCCGACGCTGTGGCCGCC
GCGGC (SEQ ID NO. 16)

.....:Rv106T7.seq:.....
GGCTNGCGTACCCGGTACCGGCCCGGGCCTACCAGTGCCGGAACCTGGAAGCGCAGTAAGCCCTCAACGCGCCACCG
CTTTGGCCCGCGCGCCCGGCGTAGGCGCATCGCGGTTGGCGTGGGGCGGCGCACTGCGACCTCACCAGCGCTTTCCG
AGCTTTGTTGATCAACCGGCCAGCATGGTCGANGATGCATTGAGACCATATTCGAAATTGGTTTCATCGGGGGCCC
CGATCCGATGCCCCCTCCAGTTGCGTGAGCAANCAGCGGAGTCNTCGCGGGATCGATGGCCACGGGGTGTCAATGG
CGGATGGTCCGCTGCCCGCCGACTGGCTCTTGCGGGAGAACCGATCTAGCACCACCGATCCGCGCACGTNG
(SEQ ID NO. 17)

Clone Rv107

.....:Rv107T7D4.seq:.....
CGTAATNTCGCGACANCCANGACTTCTGGGGGGATCNGCTGACAGTGGTNGGATCCCAAATTGCGGATGATCGGGCC
GCCNACGTCGTTGTGTACCTCNCNGTCACAACNAANCCGAANCATGACTCGGTCCACGCGGTGCGGCACATGGTG
GACACCACACCGCCACCGCNCGGGGTGAAGGCCTATGTACCGGTCCGGCAACACTCAATGCCGACGAGCGCGANGCC
GGACACANAGTATCNCCTAACGTACCCGCGATCACGAGCATGGTGATCGNNCAATGTTNCTANTGATCTATCGCTCCG
TAATTACCGCGGTTCTCGTCTTGATCATGGTCGCANCGAACTCCGGCGCAATCCGCGGATTTCATCGNCTTGCTCGCCG
ATCACATATTTTCAGCCTTTCACATTGCAACNAACCTGCTCGTCTCATGGNGATGGGGCGACACGACTACCGATATC
ATGCTCGCCGTTACACAATCNCGCCACGCCGCAAGACNGGAAACGTTCTACACAATNTTNCNGGGACGCCACTNAA
CTTGTTTCNGGTTTGACATTGCCGCGCATGNTGCCAGCTTTGCCGGCTCCCTTA (SEQ ID NO. 18)

Clone Rv108

.....:Rv108T7D4.seq:.....
TGAATTTCCCGATCCCAATCTCGGTTGAGATACAGGTCGCCATACCCCTTACTTCGGCAACGCTGGGCGGATTGGC
CCTGCNGTGCAGCANACCATCGACGCCATCGAATTGCCGGCAATCTCGTTCAGCCAATCCATACCCATCGACATTCC
GCCGATCGACATCCCGGCCTTCNCCCTTTAACGG (SEQ ID NO. 19)

Clone Rv109

.....Rv109SP6.seq:.....
AACAGCTATGACCATGNTTACGCCAAGCTATTTAGGTAACACTATANAATACTCAAGCTTTTACGGTGATCGCGCATC
ACCTGGTTCATGAACTGGAAGCAGCGCANCCTTCTTTTCGGCCGCAACATGAGCCAGCCTCTCGTCCGCGGTCTCGG
TGCAGGTGCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCCTGAAACCAGCTTCCATATCCCGCGACNAACNACNCC
AGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACAGCGCGTTCTCCACCGACCGGGCCCGGGTGTGGGGTGT
TTCCGGCGACCGGCAGGAGGTGGTCCACTGCCGACGGGCGCCGAGCCGTTACCGACCAAGCCGCCGAACAAGT
CCGCCCCGATCGCATACTCCAACCGGTTGCGGTACTGCAGGTGAGTGGCGTACCTCCTCNCGCTCGGCGAAGTCT
TGCTCCANACGTCGCGAAGCGCAAGGAACACGTTCA (SEQ ID NO. 20)

.....Rv109T7.seq:.....
GACCGNNCCATGTTCCACAATGTGGTGCCAGTNCGGNGGCTACGTGCCATCNANACACTGGCGCAGGCTATCGCACC
CGTTATCNGCTACGAACAAATCNCGGTATGCGTTCTTTANCATGAGTGGCGACCGNCGATCATGGTTCGACACCCACG
ACNGAAATACGCAGATCGCCNTCNAGCNTGTGTGCCGCGGATTATCANGACTGACCTCCTGGCTGACCGGNNTGTNTG
GTCCGCGATGCTGCGCCCCGGCCGGCGTGTGTCGTGGTTCGGATAGCGAAGTCAGCTAATTCTCGTGGCAGCTCG
AAAGGGTCTGCGGTCGCGGTCTTTGCGCAAACCATGCNCATGTTACGGTCCCTCGGGTGGCGCTGGCGGCGGC
(SEQ ID NO. 21)

Clone Rv10

.....Rv10SP6D2.seq:.....
GGGATGGGCGGGCCGCTAAACTCTTCGTGTTCCACTAACTCCGGGAGGGNCAATCTCGGGCCGTTATGGCTCACGTC
GCGTCGCCCTCCGACCGCAACATTCCGAGTTGGCAGCAACCTGGTAGCACCTGGCCGG (SEQ ID NO. 22)

.....Rv10T7D4.seq:.....
NCCGTCGTTGACAAGTAAATATGTCCGAAAAGTCTCAGCGGCCGACTTTGCTCGCAGGTGGCGGTACCGCGCCACCG
AGTCGATGCCGTGGTTCGCGGAAGAATGCCTCCCGAAATCGCACGGCTTCCCNNTTTAAACGGA (SEQ ID NO. 23)

Clone Rv110

.....Rv110SP6.seq:.....
TTTAGGTGACACTATAGAATACTCAAGCTTTTGGTCTAGCCGGCCGAGCAGGATACGGGTGTCATTGGCCACCGGCGG
CGGCTGTCCGGGAAATGGCGGGTCCCCGGTGGTTTGGCTGATGAGTGCTGAACCGTANTCGAAGTGGGCGGCGTCAGA
CTCCACCCANCCAGCAGGCAGCGCGAAGCTGAATCCTCCAACCGGGTGTGTCNATCCGGACAAGTTGGGGTTCGTTTGG
GGCAATGACAGGTGGCNGCGGTGCGTTCGGGTCCGCCGGCGGAAGTGCTGCGTTGGGATCNCCTGGGATTTCGGC
NTTTTTCGGCGGGCGGTGGTNGGGGGGCAACAGGTNTCCNNGTGGGGTGGCGCTCAACGGTCNACGGCGCAAGCCG
CCGTTGTTGGTACCNGGGGCGTGGCTCCGGATCGCGTTGGCGGTNCNCGG (SEQ ID NO. 24)

.....Rv110T7.seq:.....
CTACACCATCGAATACGACGGCGTCCGCCNACTTTCCGCGGTACCGCTCAACTTTGTGTCGACCCTCAACGCCATTGC
CGGCACCTACTACGTGCACTCCAATACTTTCATCCTGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATAC
GGTCGGTCCCAGATGACCCAGTACTACATCATTCGACGGANAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCC
GATCGTGGGGAACCCACTGGCGAACCTGGTTCAACCAAACCTGAANGTGATTGTTAACCTGGGCTACNGCGACCCGGC
CTATGGTTATTNCNACCTCNCGCCCAATGTTGCGACTCCGTTCCGGTTGTTCCANAAGTCNNCCCGGTGCTCATCGC
CGAANCTCTCNTCCGGGACCCACAGGGAATCNGCNATTTCCNCTACAAATCANCCACCTCCA (SEQ ID NO. 25)

Clone Rv111

.....Rv111T7.seq:.....
GCATGATCGGCCACCTTTCCGGCCGCCCGGCATACGGCGGCGTACCGATCTCCGCGTCATACACCGCGGGTAATCGC
CGACGGTGCCGGTTCCGAGCCGAAGGTGACGACTCTGATTGAATCGAGTTCCAGGTCCAGCGGGTGGCGCACCAACG
GCGCGAGCTCAACGACGTCATCNCGTTGTCGCTTTCTACGGTCACCGACCTGGTGACCGTAGTTCNCCCG
(SEQ ID NO. 26)

Clone Rv112

.....Rv112SP6.seq:.....
GACACTATAGAATACTCAAGCTTGCCAACCGCCAGCCTGCATCCGGCGGCGANCACTGCTCCGCCGACCAGTACGAAC
CAACCTGCGGTGCCCAGGCCATTGACGATGTGCTGGTCCGGCGCCCGCGAGTCCGCGCACCATCAACGCCGCGGGCACC
ACCANGGCGGCCCCACCTGCAAGCGGACGATCATTCGGCGCCGCTCACGGCGGGCGGGGCTCGAACANGCACAGCA
TCAACGTNGTCACCGGCCGTGACCGGCCCGCATCGTCACACCAACCAAGCCATTGCGGTCTCTCTCAACNGGGCGA
CCCGGCCCGCATCGTCACAGGNCTAAGGCCATTGCCGTCTCTCT (SEQ ID NO. 27)

.....Rv112T7.seq:.....

TCGGCGCCATCGGCACCTTCGAGGACCTGTATTTGACGCGCGTGGCCNACCTGAGGTTGGCGGTGGACNAAGTGTGCA
CCCGGTTGATTTCGCTCGGCCTTGCCGGATGCCACCCNCGCCTGGTGGTTCGATCCGCNAANAGACAANTTGTGGTGGA
NGCTTCTGCTGCTGCGACACCCACNACGTGGTGGCACCGGGCAGCTTTAGCTGGCATGTCCTGACCGCGCTGGCCGA
CNACTCCAGACNTTCCACNAANGGTGCGCNCNCCCAATGTNCCGNANTGTCTCCGGNTCCCTTTACCNCCCAATGGGCN
GNTTCCACNGGTTACGGGCCCCNTNCCGGCGGGTCTNCTCCCAANTACCAAATACGCCCGACNTTCCGGA

(SEQ ID NO. 28)

Clone Rv113

:::Rv113SP6.seq:::

ATACTCAAGCTTTTATGGTGATCGCGCATCACCTGGTTCATGAAGTGAAGCAGCGCAGCGCTTCCTTTTCGGCCGCA
ACATGAGCCAGCCTCTCGTCGGCGGTGGGTGCGAGGTGCTCGGGCAGCTCGGCCGCGAACAGCCCGGCTTGAACCTG
AAAACNGCTTTTCATATCCCGCGACGAAAGAACGCCAGTTCCGCTACTTAACCCCTCCGCGAACCGTCCATGGACAA
CAGCGCGTTCTCCACCAACCGGGCCCGGT (SEQ ID NO. 29)

:::Rv113T7.seq:::

TCGGCTCAGGCCGCGCTGCTGGTAGAGTCGTCGACCGGTGCGAGTTTCGACAATGTGGTGCCGGTTTCGGCGGCTACGT
GCCATCGAGACACTGGCGCAGGCTATCGCACCCGTTATCGGCTACGAAGCAAATCGCGGTATGCGTTCTTGAGCATGA
GTCGGCGACCGTCTCATGGTCGACACCCACGACGGAAGACGCAGATCGCCGTCAAGCATGTGTGCCGCGGATTATC
AGGACTGACCTCCTGGCTGACCGGCATGTTGGTTCGCGATGCCTGGCGCCCGGCCGGCGTGGTCTGGTTCGGCTCGGA
TAGCGAGGTGACGCAATTCTCGTGGCAGCTCGAAAGGTCCTGCCGGTGCCGGTCTTTGCGCAAACAATAGCGCAGGT
TACGGTTCGCGCGGGTGCGGCCTGGCGGCGGCC (SEQ ID NO. 30)

Clone Rv114

:::Rv114SP6.seq:::

CAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTCGCGTCTACGCCGGCCCGGAGCATCCGCACAGCGCTCAGCA
GCCGGTTCCGTACGANCTCAAGCAGGTGGCGCAATGACCGAAACACCCAGCCCGCAAACCCGGCGGCCCGGCC
GGGCCCCGACAATCGTTCTGTTGGAGCGGCCCATCCANACCGTTGGCGCCGTAAGGANGCGGTGGTACGAATGCGG
CTGGTGCCCGGCACCGCAAGTTCGACCTCAACGGCCGCGAGCTTGGANGACTACTTCCCAAACAAGGTGCACCAGCAG
TTGATCAAGGCACCCCTGGTCACCGTGGATCGGGTGAAAGTTTCGACATCTTTGCCACCTGGGCGGCGGCGGCCGT
CCGCTCAGGCCGGGCTGCCCTGGGTATCGCCGGGCATTGATTCTGGTATCCCNAGAAGAACG (SEQ ID NO. 31)

:::Rv114T7.seq:::

CGGTTGGCCACCGCTTCGCGGTGCGCGCCCGTTCGACAATGACCGTGTCTGCTGCTGACCAACACGCGTCGGGCC
GAGCCAGCACCTCCAAGCCACCTCGCGCAGCACCATGCCGCGTTCGGGGTTGACCACTGGCCACCCGTCACCACC
GCCAGGTCTCAAGGAAACGCCTTACGGCGGTACCGAAGTACGGCCCTTGACCGCGACCGCTTCAACGTCTTGCG
AATCGCGTTGACGACCGCTCGCCAACGCTTCGCCCTCCACGTCTTCAGCCACGATCAGTAGTGGCTTACCCGTTCC
TGCAACCTTTTCAGCAATGGCAACAGATCGGGAAGCGANCTGATCTTGTCTTGGTGCN (SEQ ID NO. 32)

Clone Rv115

:::Rv115SP6.seq:::

CCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTTTGGCTGGGTGCGCTTCGAATTCNGCGTGACCGCTATGG
GTTGCANAGCGGCTGGCGCCGACACCCACTGGCCCGGGTGTTCGCCCGAACC CGGATCATGGTGAGCGAAAA
GGANATTNCCTGTTGATGCTGGGATTCGCCACGCCAAGGCATCTANCGATTACTCTCNCGGGTGGGAAAAGTGC
CCAATCCCCCTCCCTCCAATTTCCNAACAATCATTCGGTTCNCNCTCCGGTTGGNGGTAACCNCCAATAAAACC
CTGCCCCG (SEQ ID NO. 33)

:::Rv115T7.seq:::

GCCCGCNCATGGCCAATCCCCGAAGACATCATTTGCCAGTGGCCGGGCGCTAACAGGTTCCAGCCCCCACCANTGCC
GCTCGAACATGCGGTGCAACCCATTTCGAGGCCGGCAGGGAAAGCACCGGGAAGCCGCAAAGGGTGCAGTTCCGCG
CCCAATAATGTCGTCGCAACCCAGATGCGCTCNAACCCNCCGCGAGTCAGCGCACCCGACCGANGTTCGAAAGAC
GTCNTCAGCGCGCCACATGGGGTGCCAATCGGCACGGCAGGTATGCCGCGCGCAACCCGAGCGGTGGTGCATGCC
ACGGTCCGCANGANGCGCANACCCGCCAATGCCGAANCCACGAAACATCGGGCGCATCCACCTTCAACC

(SEQ ID NO. 34)

Clone Rv116

:::Rv116SP6.seq:::

ATACTCAAGCTTGCCGCGCTCGATGACAAGAAATATGTCGCAAAAGACTCAGCGGCCGACTTTGCTCGCAGCTGG
CGGTACCGCGCCACCGAGTCGATGCCGTGGTTCGCGGAAGAATGCCTCCCGAATTTCGCACGGCCAATTCATTCCGGGA
AGCATCCGCAATGCCAGCTGCGGTTGCCCCCTGCCGGCCACGGCACCCACTTGCGGCATTGCGTCCACCTGGGCCAGC
GCCCGCGGCCAATTCCAAACAATAAAAATTGCACCCGGC (SEQ ID NO. 35)

.....Rv116T7.seq:.....
CCACCCGTGTATTTTGGGATGGGCAAAAAGGCGAAGCACCGCGTGGCCACGAACGCCGGGAGGGACAATCTCGGGCGG
CTAGGGCTTCTCGCGGGAAGGCCGAACGTACGGCGTTTCAACACGTGCGCTCGCCCTCCGACCGCGAACATTGCGGG
ATGGCAGCAACCTGGTAGCACCTGGCCGGGCGATGATCTGCAGCGTCGCCGCGGGTAGTCGCCGCCGGGCGGCTAC
AGTCTGAAACGCGATGACCATCGATGTGTGGATGCAGCATCCGACGCAACGGTTCTACACGGCGATATGTTGCGCTC
CCTGCCCCGT (SEQ ID NO. 36)

Clone Rv117

.....Rv117SP6D2.seq:.....
CTGCCCATTGTTTGGGGACGCCGACCAGCCGATGTGAGGCGCTACACGGCCCTTGGTGGCTGGCCACGGCGACCGA
GCGGCTGCAACTGGGCGCGTTGGTGACCGGCAATACCTACCGCAGCCNGACCCCTNTCNCAANAGGATNTTGTTCGCC
GGACCCCNCTC (SEQ ID NO. 37)

.....Rv117T7D4.seq:.....
CCGACTTTCGCGGTACCCGCTCAACTTTGTGTCGACCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCA
ACTTCATCTGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGACCCAGTACT
ACATCATTGCGACGGAGAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACC
TGGTTCAACCAACTTGAAGGTGATTGTTAACCTGGGCTACGCGACCGCCTTT (SEQ ID NO. 38)

Clone Rv118

.....Rv118SP6.seq:.....
ATACTCAAGCTTTGTACACCAAGTGTTCGACCAGGCGCTCCATCCGGCGAGTGGATACTCCAGCAGGTAGCAGGT
CGCCACCACGCTGGTCAGTGCAGCGTTCAGCTCGCTTGCAGCGCTGCAGCAGCCATTGCGGGAAATACCTGCCCTGGCG
CAGCTGGGGGATCCCAACTTCAATGGTTGCGGCACGGGTGTCAAATTCAGGTTGGCGGTAGCCGTTGCCCTAATTGGA
CCGCTCATCGCTGCTTTCGCGGTACCCCGCCCGCACAGGGCTTCGGCTTCAGCCCCATCAGGGCGGCAATAAACTT
CAAGAGCACC (SEQ ID NO. 39)

.....Rv118T7.seq:.....
GAGGCAGCTTCGCCGGCAATTCTACTAGCGAGAAGTCTGGCCCCGATACGGATCTGACCGAAGTCGCTGCGGTGCAGCC
CACCCTCATTGGCGATGGCGCCGACGATGGCGCCTGGACCGATCTTGTGCCGCTTGCCGACGGCGACGCGGTAGGTGG
TCAAGTCCGGTCTACGCTTGGGCCTTTGCGGACGGTCCCGACGCTGGTCGCGGTTGCGCCGCGAAAGCGGCGGGTCGG
GTGCCATCAGGAATGCCTCACCGCCGCGGCACTGCACGGCCAGTGCCGCGGCGATGTCAGCCATCGGGACATCATGCT
CGCGTTCATACTCCTCGACCACTCGGCGGAACAGCTCGATTCCCGGACCGCCAGCGCATTTGGTGATGGAATCGGCGA
ACTTGGCCACCCGCTGGGTGTTGACATCCTCGACGGTGGGCAATTGCGCCTCGGTAAGCTTTCGCCGCTAGCCTTTTC
ATC (SEQ ID NO. 40)

Clone Rv119

.....Rv119SP6.seq:.....
ATACTCAAGCTTCACTGACAAGGGACGAATTCGTGCGCCGCCTGTTGACTGGGTGGTGGCCGAGCTGGTCGCCACCA
CTCAGGCCGCGGTACGCGCGGTACCGGCGCGGGAGCAAATCGCGCGGGCATGGCCAATTCTTGCGGACCATCACCG
CAGACGCCCGCTTCGGACCCCTGCTGTCCACCACACAGTTGGCCAACGCATTAATCACCCGCAAGCTTGCGGAATCCA
CCGCCCTGTTGCG (SEQ ID NO. 41)

.....Rv119T7.seq:.....
TCCATCACCCGATGTGGCNGGAGCACTGCCATGTGATCTCAACTACCACCTCCGGCCGTGGCGGTTGCGCGCCCCGG
GGGTTCCGCGCGAACTCGACGAGGCGGTGCGGAGAAATCGCCNACCCCGCTGAACCGCGACCAACCCGCTGTGGGAGA
TGTAATTCGTTGAGGGGCTTGCCAACCAACCGGATCGCGGTGGTTGCCAAAATTACCATGCGTTGGCTGACGGTGTG
CCTCGGCAACATGATGGCACGGGGATGGATCTGCCGCGGGACCGGAGGTGCGCCGCTATGTGCTGACCCCGCTC
CTACCAAGCGGCA (SEQ ID NO. 42)

Clone Rv11

.....Rv11SP6.seq:.....
AGCTTTGCAGTTGCTGAGTAATGTCGGCCAACGTCAACACAACCGCGATGAATTCAATCATGCCGCCAGGGCGGGCA
ACCAATGGTGGCCGCGAGCGGAGTTCGATCGCAGCGGAGGTTGCCGCGCCAGTTGATTACGAACAGGGTGA
GGTCATAGGCGGGCAGGATAGTGACGAAGGCAAGACCTCCATCTGCCGTGGAAGAAGTATCGAG (SEQ ID NO. 43)

::::::::::::Rv11T7.seq::::::::::::
AGCTTCAGAACAGGCCTGTTGTGGGCGCACCCGGCTCGCCGAGTTCTGCACGCACCCGCTCAAGTGCGGCCCCGCACCG
CCGGCATCTCCCGGTACGCGAGGGCCGCGGCCCGCGCCGACGCGACGGCGTGTTCGCGCAGTTCCCGGTCAATGATGC
TGACCTGATCGGCCACCCGGGCGTTCTCGGCGTCGTCGCGTTCACTAATCGCGGTCTCAGCAGCGTCTCGACAGCCA
CCACCCGAGTGCGGACACAGCTGCTCCACCACGGACCGCAGCGATGCCCGTC (SEQ ID NO. 44)

Clone Rv120

::::::::::::Rv120SP6.seq::::::::::::
ATACTCAAGCTTCAGTTCTCCACGACGCGTTCCCAAATGAATTTCCCGATCCCACAATCTCGGTTCAAGATACAGGTC
GCCATACCCCTTACTTCGGCAACGCTGGGCGGATTGGCCCTGCCGCTGCACCAAACCATCAACGCCTTCAAATTGCCG
GCAATCTCGTTCAAGCAATCCAT (SEQ ID NO. 45)

::::::::::::Rv120T7.seq::::::::::::
GCTCTACGCCGCTACGGGTGGAACATGCATCCCGAGCAGATGCTCGAGCGCGCACCCCACTCGCCGATGGCCGGAAC
CGGCTGGTTACCCGGGTGGCGGCTGACGTTCCGGCGCGAGGACATCNGCTGGGAAGGGGCGCTTGCCACCGTTCGTCTCNA
AGACCCAAATTCGAAGGTGTTGCTCGTCTCTACGACATGACCCCGGCGGACGAGAAGAACCTTGACCGGTGGGAAGG
CTCCGAGTTCCGGTATCCACCAGAAGATCCGATGCCGCGTGGAGCGATTTCCTCGGACACCACAACGGGATCCCGTCC
TCG (SEQ ID NO. 46)

Clone Rv121

::::::::::::Rv121SP6.seq::::::::::::
ATACTCAAGCTTGCCAAAGACCTCGTCCACCAAGCAGGACGCGACCGTCGAGGTGGCGATCCGGCTTGCGGTCGAC
CCGCGTAAGGCAAACAGATGGTTTCGCGGCACGGTCAACCTGCCACACCCGCACTGGTTAAGAACTGCCCGCGTCGC
GGTTTTTCGCGGTTGGTGAAAAGGCCAATGCCGCGTTTGCCGTGGGGCGGATGTTGTGCGGAGTGACAATCTGATCA
AAAGGATTACGGGCGGTTGGCTGGAATTCATGCCGAATCGCGACACCGG (SEQ ID NO. 47)

::::::::::::Rv121T7.seq::::::::::::
CCACGGCGTGGATCAAGGTACCGGCCGGGATGTTGCGCAATGGCAGGTTGTTGCCCGGCTTGATGTCGGCGTTAGCGC
CGGATTCACACATCCCTTGCAGAAAGTCCGTTGGGTGCAATGATGTAGCGCTTCTCCCCATCGAGATAGTGGAGCA
ACGCAATCCGTGCGGTACGGTTCCGGTCTACTCGATGTGCGCGACCTTGGCGTTGACACCATCTTTGTCATTGCGGC
GAAAGTCGATCATCCGTAAGCGCGCTTATGACCGCCGCTTTGTGCCGGGTGGAATCCGGCCATGCGCGTTGCGTC
CACCGCGACGTGCAGCGGGCGCACACGAGCTTCTCCGGGGTTGACCGGGTNATCTC (SEQ ID NO. 48)

Clone Rv122

::::::::::::Rv122SP6D2.seq::::::::::::
GCAGCATGACGGCGGTAGCGAACACCGCCGGATGCAGCGCAAGTAGCGTCGATGTGCTACGGAATCGCCCCGGCACC
GCGATCTCGANGATCACCAGTGCCACCCCTGCAGCGCNACACCGACGATTCCGTACACCGCCACGCCGATCAGGCCC
TGGGCCATCTGATTGGAGCTGGCGTANATGGCGGCGATGGTGACGATGGCCAGCGCCACATACATTGTGGCGGCCAGA
ACCACGGCGTTGGGGCGGCGGTGATGAACACTAGGCGACGCGATCGCCCGGGGTCAACAGGTTGACCATCAGAAAG
CCTGCGACTAGCACGGCGGCGCCACTAGGAAGTACAAGAANGTGGCCACCACCCCATGCAGGATCGGGGTAAAGGCTGA
TGGTCCCGAAATCGACTCCGGCCTAATACATGACTCTCTCTTTGCGTCATCGCCTTACTTGTGCGCGGAA
(SEQ ID NO. 49)

Clone Rv

::::::::::::Rv123SP6D2.seq::::::::::::
GGGACACACCTCGATGCTGCCGCGNATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGGAACGC
TTCCGCGCGGGCGTGACGCATCCCGTTGACCGGCCGGANCTCTCTA (SEQ ID NO. 50)

::::::::::::Rv123T7D4.seq::::::::::::
TGGGCGCCTCTTTCCGCTTCCNNTTAAACGNAGCANGACATTCTGGGTATCGAGTTGTAAGTGGATGGTGTGGCG
ATGTGCGGTGATCCTGCTCCTGGCGGTGGGATCCGACTACAATCTGCTGCTGATTTCCCGGTTGAAAGAGGAAATTGGG
GCCGATTGAACACCGGAATTATCCGTGCCATGGCTGGTACCGGGGAGTGGTGACGGCTGCCGGCATGGTGTTCGCC
GTTACCATGTCGTTGTTGTGTTACGCGATTTGCGAATTATTGGTCAGATCGGTACCACCATCGCCTTCCC
(SEQ ID NO. 51)

Clone Rv124

::::::::::::Rv124SP6D2.seq::::::::::::
CCGATCGGCGCCGCANCTGGTTGGTGTTCGGATGAATCCGCGAGCGAAAATGTAGCTGCGGTGGCGTGTGCTGACTCG
TNGGCGTCGACGCTCGTGGCAGCCACCGANCGGTTGGTCCAGGATCTGGATGGGCAAAGTTGTGCGGCCCGGCCGGT

ACGGCCGATGAGCTGACCGAGGTCGACAGCGCCGTGTTGGCTGACTTGAACCGACATGGAGTCGCCCCGGTTGGCGT
CACCTCAAGCATTTCAATGGTTATGCGACCAAGTTTGGGTTACGCCGTCAGACATCACGTCGGAGACTTGGATGAGC
TGTGTCTGCCAGATAGCCCCGAATCGGGACGACCGTGGTCACGGTGCGTCTGACCACTCGGGTCGGGTCGCCCCGCGT
ATCGGCATGGGTGCGTNATCACAGCGACGCGCTGCCAAGGANGTNCGGNCGGACC (SEQ ID NO. 52)

::::::::::::Rv124T7D4.seq::::::::::::
CGGGTTGCGGATCCACGCGTGCGGGTTGTCAGCAGCTACGGCACTGAACCGCGCCACAGCTCGCCGATCCGCTTTTCG
GTGGTTCTCGATCGACTCGCCGTAGGCGATGCGCAGCGCCTGCTCGAATATCGGGTACACGTAGGCCGGCCTTCCNC
TTTA (SEQ ID NO. 53)

Clone Rv126

::::::::::::Rv126SP6.seq::::::::::::
CTTGATTTTGATCATCATGACGATCATCACCTAATTTTGTACCCGCACTGGTTATCGTGGGTACCGTCGTGCTTTC
CATGGGCGCCTCTTTCGGGCTTTCCGTATTGGTCTGGCAGGACATTCTGGGTATCGATTGTACTGGATGGTGTGGC
GATGTCGGTGATCCTGCTCCTGGCGGTGGGATCCGACTACAATCTGCTGCTGATTCCCGGTTGAAAAGGAAATTGG
GGCCGGATTGAACACCGGAATTATCCGTGCCATGGCTGGTACCGGGGAGTGGTGACGGCTGCCGGCATGGTGT
(SEQ ID NO. 54)

::::::::::::Rv126T7.seq::::::::::::
GGGGATCCCTAGATCGACCTGCAGGCATGCAAGCTTGGCGTGTCTTCCAACCCGAATTGGCTTTTCGGCGCCATCGGT
GAGGCGGGACACACCTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGG
AACGCTTCCGCGCGGGCGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGACGGCATCGCCACCG
GAGCNACTGTCAAGGCGCGGTGCCAGGTGCCCCGGGCGCACGGTGCGGACAAGGTGGTGTGGCGGTCCCGATCGGCC
CAGACGACATCGTGGCGAGATTGNCGGGTACGCCGATGAGGTGGTGTGTTTGGCGACGCCGGGCTNGTTCTTCGCCG
NCGGGCANGGTTACCGCAACTTCAACCGACCTCCGACGACGAGGTGGTGGCGTCTCTGGATCGTGCTC
(SEQ ID NO. 55)

Clone Rv127

::::::::::::Rv127SP6.seq::::::::::::
AAGGCTGCAGGTGCAAGCGGNTGGTTACGACTCCCTGTGTGTGATGGACCAGTTCTACTATCTGCGTCTACACGGCCC
TTGGTGCGCTGGCCACGGCGACCGAGCGCTGCAACTGGGCGCGTTGGTGACCGGCAATACCTACCGCAGCCCCGACC
CTGCTGGCAAAGATNATCACACGCTCGACGTGGTTAGCGCCGGTCGAGCGATCCTCGGCATTGGAGCCGGCGGGTTT
GAACTGGAACACCGCCAGCTCGGCTTCGAGTCCGGCACTTCCAGTGACCGGTTCAACCGGCTCGA (SEQ ID NO. 56)

::::::::::::Rv127T7.seq::::::::::::
CTTTCGGCGGTACCCGCTCACTTTGTGTCGACCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAATACTT
CATCCTGACGCCGGAACAAATTGACGNGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGACCCAGTACTACAT
CATTCGCACGGAGAACCTGCCGCTGTACAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGGT
TCAACCAAATTGAAGGTGATTGTTAACCTGGGCTACGGCGACCCGGCCTATGGTTATTGACCTCGCCGNCCAATGT
TGCGACTCCGTTTCGGGTTGTTCCAGANGTCAGCCCGGTGTCATCGCCGACGCTCTCGTCN (SEQ ID NO. 57)

Clone Rv128

::::::::::::Rv128SP6.seq::::::::::::
CGGTATAGCCCTCGGGTCCGGCCAGCACTCCGACGGCTTCGTGGGGTGGTCGCGACGCGCATGGGCCACCATCGCA
TTCACCAAGTCTGCGCGAATCACAGCACGTAGACGGTTCTTTCTAAGCAACACCGAAGTTTCAGACCCGAATGC
TCCGGGAACATGTACGGTAGGTGCGTATTCGGCTACCGGCTGAGCATTGAGCACGCGCGGACACCGCACGAGC
CAGGCAATCAGCCGCCCGCCGACCGATCGCGGTGACAGCTGAGTCTCCGAGACAATGCGGCCGCGACCCGGNCTC
CGCGGCACCGCTACNGCGCCCGTGG (SEQ ID NO. 58)

::::::::::::Rv128T7.seq::::::::::::
GTGATGGCACGCCACCGACACACCGGCTGCGTACNTCGAGCCATACCGGGCGGAGCTACATCGGCTCGGCCG
CCAGTGTTTCGGGCCCTCTTTCGAGGTGAGGTGATACCGATTGCGCATCCGCANCCGNCCTGGACGACAGAACC
GTGCCCTACGAGTGCTTGTGGGCGGGGCCAAAGAACAGCTTGGCATCTGGCGCGATTGGCCGCGCGCGCTGGT
GCCAAGGACGACGCCGTTCCGGTGTGATCGACGACGCGTGGGGTTACCGATCCGGAGCGACTATCAAGATGGGG
AGGTCTTGACACCATCGGCCCNACGGACATGTGATCGTCCGACGTGAGTCCCACCCG (SEQ ID NO. 59)

Clone Rv129

::::::::::::Rv129SP6.seq::::::::::::
GCGAAAGTCCGTTGGGTGCAATGATGTAGCGCTTCTCCCATCGAGATAGTGGAGCAACGCAATCCGTGCGGTACGGT
TCGGGTGCTACTCGATGTGCGGACCTTGGCGTTGACACCATCTTTGTATTGCGGCGAAAGTCGATCATCCGGTNNG

CGCGCTTATGACCGCCGCTTTGTGCCGGGTGGTAATCCGGCCATGCGCGTTGCGTCCACCGCGACCGTGCAGCGGGC
GCACCGAGCGACTTCTCCGGGGTTGACCGGGTGATCTCGGCGAAATCAGATACGCTGGCGCCGCGACGACCGAGCGCTCG
TGGGCTTGTNCTTGCGAATTGNCATGTCTAATCANGTCTTTCTCTACGCTCTCGTCGCCGGGGCTAGGCCGCAATTGCC
CTGCTCCTCCTCATCGCTTCGCTCTGCATCGTCCCCGGGCTAAGCCCGTGCCCCGAAA (SEQ ID NO. 60)

::::::::::Rv129T7.seq::::::::::
GATGGTTGCGGGCAGGTC AACCTGCCACACGGCACTGGTAAGACTGCCCGCGTCGCGGTATTGCGGGTTGGTGAAAA
GGCCGATGCTGCCGTTGCCGCGGGGGCGGATGTTGTGGGAGTGACGATCTGATCGAGAGGATTACAGGGCGGCTGGCT
GGAATTCGATGCCGCGATCGCGAACACCGGATCAGAATGGCCAAAGTCGGTCGCATCGCTCGGGTGCTGGGTCCGCGC
GGCCTGATGCCCAACCGAAAACCGGCACCGTCACCGCCGACTCCCCATGGCGTCCCGGATATCAAGGGCCGGCAAAT
CAACTTCCCGGTTGATCAGCAAGGCAACCTGCCTCNCCTCCGG (SEQ ID NO. 61)

Clone Rv130

::::::::::Rv130SP6.seq::::::::::
ATACTCAAGCTTCGTCATAAGACCATGGTGCGCTTTCTTTACCCCGTCCAGAGTCGGGGGCATCCGCACCGGCTCGCA
TCGCATCATCTCCACGACGGGCCGCTCATCAGCTTGGGCCATTTCAATGTACTTGATAACCCGCGCTGCGGGTAGG
CCACTGCGACAATTCAAACACGGTGTACACGGTGAATAGTGTGAGATGGGCTCTGATCAACCGTCGCAAAACCGGT
TTCGCATCAATAGCGGAATCCACCGGGTTGCATGGAGGCTGCTGACCTTGAAAAACAAATTTTTTCATTACAACAA
AACACCGCCNCGGAACTTTGCA (SEQ ID NO. 62)

::::::::::Rv130T7.seq::::::::::
CGAATTCGGCGTGACCGCTATGGGTTGCAGCAGCGGCTGGCGCCGCACACCCCACTGGCCCGGGTGTTCGCCCCG
AACCCGGATCATGGTGAGCGAAAAGGAGATTGCGCTGTTGATGCTGGGATTGCCACCGCGAGGCCATCGACCGATT
ACTCGCCACCGGGGTGCGAGAGGTGCCCGAGTCCCGCTCCGTCGACGCTCTCCGACGATCCATCCGGCTTCGCGCTCG
GGTGGCGGTAGCCGTCGATGAAATCGCTGCCGGCCGCTACCTGCAAGGTGATTCTGTCCCGTTGTGTGCAAGTGCCCT
TCGCGATCGACTTTCCGTTGACCTACCGGCTGGGGCTCGGCACAACACCCCGGTGAGGTCGTTTTTGTGCAAGTGCTG
GCGGAATCCGTGCTCTGGGTTACAGCCCCGAACCTGTCACGGCGGTGCGCGCCGACGGAGTTGTTATACCGATCCGT
TGGCGGTACCGCGCCTTGGGC (SEQ ID NO. 63)

Clone Rv132

::::::::::Rv132SP6.seq::::::::::
TCAGACTCCACCCAGCCAGCAGCGAGCGAAGCTGAATCCTCCAACCGGGTTGTCGATCCGGACAGGTTGGGGTGCG
TTTGGGGCAATGACAGGTGGCGGCGGTGCGTTCCGGTCCGCCGGCGGAGGTGCTGCGTTGGGATCGCCCGGCTGGGCA
TTTCNGCGTGTGGCGGGCGGCGGTGGTGGGGGGCAACAGGTGTCGCCGCTGCGGGTGGCGTGCAGCGGTGACGGC
GGCGAAGCGGCGGTTGTGGGTACCGGGGGCGCTGCTCCGGATCGGCGTTGGCGGTGCGGGGACCGCAACGGTCACC
AAGCTGGCGCTGGCCATCGCCGCGATAGCCAGTGCCGCCAATCGTCCCTTGCGACGTGTCAAGTNGGGGTCCACCTGA
TGCATGGCCAAAGAACCTACCGTGTTAACGGCNCAACNCAAGGACCGCGCCGGTCCGN (SEQ ID NO. 64)

::::::::::Rv132T7.seq::::::::::
TTTCCGCGGTACCGCTCACTTTGTGTNACCTCAACGCCATTGCCGGCACCTACTACGTNCACTCCAACCTACTTC
ATCCTGACGCCGGAACAAATTGACGCGAGCGGGTCCGCTGAACAATTCGGTCCGTCCCACGAAAGAACAGTTTNCNT
CTTTCNCACGGAGAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGTG
TTTCAACCAACACTTAGAGTGTAATTGTAAACCTGGGCTAGGGGAAACCGGCTCTAGTTTTTCCACNTCTCCGCCCC
NTGTTTCGAATACTCCGTTCCGGTTGTCCCAAA (SEQ ID NO. 65)

Clone Rv134

::::::::::Rv134SP6.seq::::::::::
GCTTCCGGCTCGTATGTTGTGTGGAATTGTGACCGGATACCAATTTACACAGGAAACAGCTATGACCATGATTACGC
CAAGCTAGTTAGGTGACACTATAACAATACTCAAGCTTGCCGGTGGTGGGCGGACCACTTCGATGGCAGACCCGTGA
ACTGCTGCCCGGCCAATTCTTCTTGGTCGCCCGGACCGATGGACCGCGGCTGGGATTCCAGAAGGTGCCGATCCGCG
CCCTGGGAAAAACCGCTGCACCTCTACTTCACGACCAACGAC (SEQ ID NO. 66)

::::::::::Rv134T7.seq::::::::::
CCGATCGACTGATGCGCCGACAACACGCCCCAACAACTGGAATGAACCGTCGTGACCATCATCAGCACGCGGTTGTA
GGCGACTTGCGACATGTTCAACCCGCGCTACTCGGACGGAATCTTCAAACCGAAACAGCCAGCTCGGCCAGGCCCTTT
CACGTAATCGTCGGGGATCTGGGCACCAAGCTCGAGGACGCTGCCGTCCACGGTGTCTAGGAATTCGCGAGTTTGAC
CAGAAACGCTCGGTTCCGGCCCTCTCGGCGTCCGACGGCTGGGAAATGGGTGTATGAGCCCTACGGGAAACCGGCC
CACAAAGAGTTCTTTGGCGAAGGACGGTTATCCCAACCACTTTCGCGAGATTCTCGGCAAGGGCCCGCGCTTGCTC
CTCGGTGACCTGAGTTGTGTGCCATCGCCGCTCCTCCCTGA (SEQ ID NO. 67)

Clone Rv135

.....Rv135SP6.seq:.....
TGCATCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACG
CCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTTACGGTGATCGCGCATCACCTGGTTCATGAACTGGAAGC
AGCGCAGCGCTTCCTTTTCGGCCGCAACATGAGCCAGCCTCTCGTCGGCGGTGCGGTGTCAGGTGCTCGGGCAGCTCGG
CCGCGACAGCCGCTGACCTGAAACCAGCTTCCATATCCCAGCAGAACGACGCCAGTCCGCTACGTAACCCCTCCG
CGACTGTCCATGGACAACAGCGCGTTCTCCACCGACCGGGCCCGGGTGTGGGGTGTTCGGCGACCGGCAGCCAGGTG
GTCCACACTGCCGACGGGCGCCGCGAGCCGTTACCGACCGAGCCGCGAGCAAGTCCGCCCGATCGCATACTCC
(SEQ ID NO. 68)

.....Rv135T7.seq:.....
GGGGGCGTGTGTTATAGTTCGCTGACCGGTGCAGGTTTCGACAATGTGGTGCCGGTTCGGCGGCTACGTGCCATCGA
GACACTGGCGCAGGCTATCGCACCCGTTATCGGCTACGAGCAAATCGCGGTATGCGTTCTTGAGCATGAGTCGGCGAC
CGTCGTTCATGGTCGACACCCACGACGGAAGACGCAGATCGCCGTCAAGCATGTGTGCCGCGGATTATCAGGACTGAC
CTCCTGGCTGACCGGCATGTTTGGTCGCGATGCTTGGCGCCCGGGCGGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGT
CAGCGAATTCTCGTGGCAGCTCGAAAGGGTCTGCGGGTGGCGGTCTTTGCGCAAACGATGGCGCAGGTTACGGTGGC
GCGGGGTGCGGCTGGCGGCGGCCAGAGCACGAGTTACCGATGCGCAGCTAGTGGCGACAGCGTCAGCCAAC
(SEQ ID NO. 69)

Clone Rv136

.....Rv136SP6.seq:.....
TGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACG
CCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTCCGTACAGGTCGCTCCAACACGGCGGGGAAGCGACACCA
GCCTACCGAGCTTGGAGTCCAGGACGCCAGCGGCGGCGTGGTCTGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT
CAACGATCTCCACCCAGCCGCTCGGGTTACCCACGATCTCGGCATAGACCGGGCCGAGGCCGCTGCGATACCGTATT
GCGTCAATTGGGACGCGGTTGTGCATTGCGCTAGCTCGGTTGCCACACCCGTCAGGGGTTGACGTTGGCGGGTTCGG
CGGGCCCCAGCACCCTGTCACCATGCCGCCAAGCCGACCTGCGGCGCCACCACT (SEQ ID NO. 70)

.....Rv136T7.seq:.....
CGGCATGACCACCGACAGGCCCGACTGGTTCGTACCACTCGAACGCCGGGGTGTGATGTCCCAGCCGCTGAAGTCGT
CTGCGCGCGCAGGCCGTCGAGCAGGTACAGGGCGGGCGAGTTGGCACCACCACTTTGGAATTGGACCTTGATGTACG
GCCCATCGACGGCGACGGCACCTGCAGGTACTCCACCGGCAAGCCCGGCGGGGAAATGCCCCCGGGTTCGCGTGGC
ACCGACGGGCGCGACAGACCCGACCTAGGGCCGCGCGGACGGCCCGACACGAGTCGACGCGACATACCCGTGAC
GGCGCCACGAACCTGTCAACAAGCTGCATTCTTGCTTCCCTCATCTCATCTCAACGCATCCATGCATGTTTGGGCG
CATCTGAATTANGTCAGACTGCAGGCGCTGGGCGGCGAGTGCTCGTGTATCAACCACAACCTTCGGGCGT
(SEQ ID NO. 71)

Clone Rv137

.....Rv137SP6.seq:.....
TTCCAACCCTAATTGGCTTTCGGCCCCATCCGTGAGGACGGGGTGGGGTGTCTCAACAACAACGTCGTCCGCGGGACA
CACCTCTATGCTGCCGCCATGGACGCGGTCCAACGCAAGCAGCTGATCGAGCTACAACCCCGCGCGGAACGCTTCCGC
CGCGGGCGTGAACGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGACGGCATCGCCACCGGAGCGACGGCC
AAGGCGGCGTGCCACGTCGCCCGGGCGCACGGTGGCGACAAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT
GTGGCGAGATTGCGCGGGTACGCCGATGAGGTGGTGTGTCTGGCGACGCCGGCGTGTCTTTCGCCCTCGGGCAGGGT
TACCGCAACTTCAC (SEQ ID NO. 72)

.....Rv137T7.seq:.....
CAGGCATGCAAGCTTTCCGCCGATACCCGCCATGTGCGGCACATCCAGGACTTCTGGGGGGATCCGCTGACAGCGGGC
GGATCCCAAAGTGCGGATGATCGGGCCGCTACGTCGTGGTGTACCTCGTCGGTAACAACGAAACCGAAGCGTATGAC
TCGGTCCACGCGGTGCGGCACATGGTGGACACCACACCGCCACCGCACGGGGTGAAGGCCTATGTACCGGTCGGCA
GCACTCAATGCCGACAGGCCGAGGCCGGAGACAAAAGTATCGCTAAGGTACCGCCGATCACNAGCATGGTGTATCGC
AGCAATGTTGCTAGTGATCTATCGCTCCGTAATTACCGCGGTTCGTCTTGATCATGGTCGGCATCGACTCGGCCAA
TCCGCGGATTTCATCGCCTTGCTCGCCGAACACAACATTTTACCTTTACATTTGACCAACCTGCTCTTCTCAT
(SEQ ID NO. 73)

Clone Rv138

.....Rv138SP6.seq:.....
CACTACTCAAGCTCTCTCNTCATTACCACCCCTGTAATTTGGGATGGGCAAAAAGGCGAAGCACCGCTTGGCCACNAA
CGCCGGGAGGGACAATCTCGGGCGGCTATGGCTTCTCCCGGAAGGCCCAACGTACGGCGTTTCAACACGTCGCGTC
GCCCTCCGACCGCAACATTCGGGGATTGGACCAACCTGNTACCACCTGGCCGGGCGATGATCTGCAGCGTCGCCG
CGGGTATCCCCGCGCGGCTACAGTCTGAAACCCCGATGACCATCGATGTGGATGACGATCCGACGCAACG
GTTCTACACGGCGGATATGTTCTCTCGCTGCGCGGTGGACCGGTGGGTCTATCCCTGAAACCGACATCCCN
(SEQ ID NO. 74)

.....Rv138T7.seq:.....
CAGGCATGCAAGCTTTTCGTCAAGTTCATTGCGCCAGCAGACCAACAAGAGCATCGGGACATACGGAGTCAACTACCCGG
CCAACGGTGATTTCTTGGCCGCCGCTGACGGCGCGAACGACGCCAGCGACCACATTAGCAGATGGCCAGCGCGTGCC
GGGCCACGAGGTTGGTGCTCGGGCGGCTACTCCCAGGGTGCGGCCGTGATCGACATCGTCACCGCCGCCACCACTGCCCG
GCCTCGGGTTACGCGAGCCGTTGCCGCCCGCAGCGGACGATCACATCGCCGCGATCGCCCTGTTTCGGGAATCCCTCGG
GCCGCGCTGGCGGGCTGATGAGCGCCCTGACCCCTCAATTGCGGTCCAAGAACATCAACCTCTGCAACAACGGCGACC
CATTTGTTTCGGACGGCAACCGGTGGCAACGCACCTAAGCTACTTGGCCGGGATGA (SEQ ID NO. 75)

Clone Rv139

.....Rv139SP6.seq:.....
GTTTATGCACTGGTTAGGTGTTCCATGAGTTTCATTCTGAACATCCTTTAATCATTGCTTTGCGTTTTTTTATTAAA
TCTTGCAATTTACTGCAAAGCAACAACAAAATCGCAAAGTCATCAAAAACCGCAAAGTTGTTTAAATAAGAGCAAC
ACGTACACAAGGAGATAAGAAGAGCACATACCTCAGTCATTATTATCACTAGCGCCCCGCCGAGCCGTGTAACCGAG
CATAGCGAGCGAACTGGCGAGGAAGCAAGAAGAACTGTTCTGTGATAGCTCTTACGCTCAGCGCAAGAAGAAATA
TCCACCGTGGGGAAAACTCCAGGTAGAGGTAC (SEQ ID NO. 76)

Clone Rv13

.....Rv13SP6.seq:.....
ATACTCAAGCTTGGGTGTAGCCGATCACCAGGAGTCNCATGATCAGCCACGTTCCGCGCCGCCCGGCATACGGTGGTG
TACCGATCTCCGCTCATACACCCGCGGGTAATCGCCGACGGTGCCGTTTCGCGAGCCGAA (SEQ ID NO. 77)

.....Rv13T7.seq:.....
AGCTTTATCGAAAGCGCGAACAGCTCGCGGCGGCCACGACGTGCTGCGTCGGATTGCCGGCGGCGAGATCAATTCCA
GGCAGCTCCCGGACAATGCGGCTCTGCTGGCCCCGAACGAAGGACTCGAGGTCAACCCCGGTGCCCGGGGTGCTGGTGC
ACCTGCCGATCGCACAGGTTGGCCCCAACCGGCCGCTTGATGCCCGGTGGCAAGCCCGGCAGTTGCCAAACCCATC
GTGATCAGGCTCGGCTCGCGAGTTCGGCGAAGAAATGTTTCGCTGATCACCTACCATCGGCCA (SEQ ID NO. 78)

Clone Rv140

.....Rv140SP6.seq:.....
TCAACACGCCGCCAGCCACCACGCGCGGTGCGGCGCGGGCCCGGCTCCAGGCTNCTCCGCTCGGTGATGGCAGC
CCACCGCGACACCACCGGCTGCGCTACGTGAGCCATACCGGGCGGAGCTACATCGGCCGCGCCAGTGTTCGG
GCCCTCTCGCCAGGTGAGGTGACACCGATTGCGCATCCGAGCCGACCCCTGCGACGACAGAACCAGCGGCCCTA
CCCACTGCTTGTGCGGCGGGGGCCAAAGAACAGCTTGNCATCCTGCCACAATTGGCCGGCGCCCG (SEQ ID NO. 79)

.....Rv140T7.seq:.....
CAGGCATGCAAGCTTCACGTCCGTACGGCTCGGGTACGCTTCGGTCGCGAGTGTCGAGTGATAGATGACGACCGGGAC
CTCGTCGGCATCTTCCATAGCCCGCCACACCTTCAGTTGCTACCGGAATCCAACCGGTAGAAGGTGGCCAGCGCTC
GGCATTGGTCATCGGGATATGCCGCTCGGGACGGTCAGAGCCCTCGGGTCCGGCCAGCACTCCGAGGCTTCGTCGGG
GTGGTCGCGACGCGCATGGGCCACCATCGCATTACCAGGTCTGCGCAATCACCAGCACGTAGACGGTTCCTTCCCT
AAGCAACAC (SEQ ID NO. 80)

Clone Rv141

.....Rv141SP6.seq:.....
AATATTCAAGCTTTTCGGCGGAAACGGACNCCTTGCGAACATTGATAACAAAATAGAAATCATTGATGGTTTGAGTCAC
CAGGCCGATCAAGCCTTCGCCGAGCCAAATTCGAATCAAGAGGCCCAAGCCCGTACCAATCAGCCCGGCAACGAGGGA
TTCCGTCNTTATCAGCCNAAATAACTGCTCTCGGGTACCACCCAAACAGCGCAATATGGCGAAAAACGGTCGCCGTTG
CACAACATTAAATGTCTCGGTATTGTTGATTAAAAAGATACCACACCAGGGCAATCCAATGAGAGCGGTAAAT
GACCGTAAAAACCTCCCGTCATCTGTTT (SEQ ID NO. 81)

.....Rv141T7.seq:.....
CAGGCATGCAAGCTTGCTGCATCTTCTGTGACTGCTCCCGAAACCTGGGGGTGTGCTGCTGTGTATGCACGGCATA
CGGACATCCTTCCCCTGATACCCGCGGTGCAACAGCCACGTGTCCATCATCAGGGGTCAACCCCGGCCAAGGGCGAC
GGCAGGCCAAGTTGCGCGACCGTTAACCTAGTGCTGTTAGCTTCATTTGCTGCGAGCAAAACAGCTGGTCGGCCGTTA
GGAAGTGAATTGAACTCAACCGATTGGTGCCGCCGTAAGTGTCCTGTCTGCGGGTGCGCTGGTGTGTCCGCGTGT
GGTAACGACGCAATGTGACCGGGGAGGTGAACCACTGGCCAGGCGTCCGCGAAAGTCCATTGCNNGGGGAAGAAG
ACAC (SEQ ID NO. 82)

Clone Rv142

.....Rv142IS1081.seq:.....
GAAAGTGGCCCAAGGTGTTGGTGAACTCGCTGGACGGTCCCCAGGATGTTGGCAGCACATTACCCGGACATGACCCG
AGCAAGACCGGACATCCTCCCATACCGTCGTCGCCGTGTACATCCGTAGCCCGTCCTGGCAGGTGCTGGGTTGAACAA
AATCAGCCCAACACCTGCCACGACGAAGAAGCGGGTTGCGCTGGCATGTCTTGTGCGCTCGGCGATCGAATTCTACGA
ATTCTTTATCTACGGGACCGCTGCGGCGCTGGTGTTCACCCCGTGTCTTCCACACCTGGATCCCAACGGTGGCCGC
CGTGGCCTCCAAGGGGACATTTGCTGTGGCGTTCCTATCCCGGCCGTTGCGCGCGGCCGTCTTTGGATACTTTGGAGA
CCGCCTCGGCCGCCAGAAGACCCTGGTCGCCACACTGTTGATCATGGGCCTGGCAACCGTGACTGTTGGGCTGGTTCC
ACGACAGTGGCCATCGCGC (SEQ ID NO. 83)

.....Rv142SP6.seq:.....
ATATTCAAGCTTTGTACACCAAGTGTTCGACCAANCGCTCCATCCGGCGAGTGGATACTCCAGCAGGTAGCAGGT
CGCCACCACGCTGGTCAGTGCCTTCATCTCGCTTGGCGCGCTGCAGCAGCCAGTCCGGGAAATAGCTGCCCTGGCG
CAGCTTGGGGATCGCGACGTCGATGGTTGCGGCACGGGTGTGAAATCACGGTGGCGGTAGCCGTTGCGCTGATTGGA
CCGCTCATCGCTGCGTTGCGGTAGCCNCCCGCACAGGGCGTGGCTTCAGCCCCATCCAGGCGGCGATGAACG
TCGAGAGCAGCCCGCGCAGCAAATCCGGGCTCGCTGTGCGAGTTGGTCAGCCAGAAGCTGCTCGGTGTCATAAGATG
AGAAGAGGTCAGTGCGTCCTTTCCTTCG (SEQ ID NO. 84)

.....Rv142T7.seq:.....
CAGGCATGCAAGCTTTTTGAGCGTCTCGCGGGGCGAGCTTCGCCGGCAATTCTACTAGCGAGAAGTCTGGCCCCGATACG
GATCTGACCGAAGTCGCTGCGGTGCAGCCACCTCATTGGCGATGGCGCCGACGATGGCGCTGGACCGATCTTGTG
CCGCTTGCCGACGGCGACCGGTAGGTGGTCAAGTCCGCTACGCTTGGGCTTTGCGGACGGTCCCGACGCTGGTC
GCGGTTGCGCCGCCAAAGCGCGGGTGGGTGCGGTGATGAATGCCCTACCGCGCCGACTGCACGGCCAGTGCCCC
GGCGATGTCAGCCATCGGGACATCATGCTCGCTTCATACTCCTCGACCACTCCGCGGAACAGCTCCATTCGGGAC
GCCCCAACGC (SEQ ID NO. 85)

Clone Rv143

.....Rv143SP6.seq:.....
ATACTCAAGCTTTTGGCTGGGTGCGCTTCCAATTGACGCTGCACCGCTATGGGTTGCAGCAGCGGCTGGCNCCGCACA
CCCCACTGGCCCCGGGTGTTTTCGCCCCGAACCCGGATCATGGTGAGCGAAAAGGAGATTNCCTGTTGATGCTGGGA
TTCGCCACCGCGAGGCCATCGACCGATTACTCGCCACCGGGGTGCGAGAGGTGCCCGAGTCCCGCTCCGTGACGCTCT
CCGACGATCCATCCGGCTTCGCGCGTGGGTGGCGGTAGCCGTCGATGAAATCGCTGCCGGCCGCTACCACAAGGTGA
TTCTGTCCCGTTGTGTCCAAGTGCTTTCGCGATCGACTTCCGTTGACCTACCGGCTGGGGCGTCGGCACAACACCC
CGGTGAGGTGCTTTTTTGTGAGTTGGGCGGAATCCGTGCTCTGGGTTACAGCCCCGAACCTCGTCACGGCGGTGCGCC
GCCGAC (SEQ ID NO. 86)

.....Rv143T7.seq:.....
CAGGCATGCAAGCTTCAACCTATTGACGCATTGTGCGAACTGACGGCGCCCGCGCATGGCCAATCCGGAAGACCATCA
TTGGCAGTGGCCGGGCGCTAACAGGTTCCAGCCCCCAGGTGCCGCTCGAACATGCGGTGCAACCCATTTCGAGG
CCGCGAGGAAAGCACCGCGGAAGCCGCAAGGGCTCGAGTTCCGCGCCCAATAGTGTGTCGCGCAACCATGCGCT
CGAAAACCGCCCGCGGCGAGTCAGCGCACCCGACGCGAGGTGAGAGACGTCGTCAGCGCGCCACATGGGGTGCCAAT
CGGCACGGCAGGTAGGCCGCGCAACCCCAACGCTGGTGCATGCCAGGTCCGCGAGGAGGCCACACCC

(SEQ ID NO. 87)

Clone Rv144

.....Rv144SP6.seq:.....
ATACTCAAGCTTCCCGGCCGAGGTGACGGCGCGGCTAGCGCCACTTGATGCCGACCCGATCGACGGNCGTTGGTC
GGGTTGACTGGCCGCGCCGCGAGCAGGGCGTCAACCGCGGCCGACGTCGGCGGCCGTACCGGTGCGCCATTGCC
CGGGCGGGAGTCGTCGAGCTGACCACGGTAGACAAGTCGGCGCTGGCCGTGCAAGACAAACGTGTGGGTGTGAGGC
CGCGGAGAAGGCGNCGGCGACGTCCTCGGTTTCGTCGTAGAGATACGGGAACGTCCAGCCGTGGCGGCGGGCTCGGC
GACCATCTGATCGGGCCGCTCCTGCGGTAGGTGACCACTCTTACTGGAGATACCGACCATCGGGACCCCTTTGATC
GGCGAGGTCCCGGCCGACCGTGGCCAATCCGGCGGCGACGTGTGCCCCGTACCGGCCAGTGTTT (SEQ ID NO. 88)

.....Rv144T7.seq:.....
CAGGCATGCAAGCTTTANCANATCAACCCCGCCCCGACACGACCGACACGATGTCGATGCCATCGAGGTGAATGT
CGAACTGGCNCAAACCATCTGGCGACCGCGACACCGGCAACATGGGTACCGCGGATTTCCGGTGCCAATGCCGACCC
GACGGGCGCTCTACCGCAGGTGACCTCGATCAGCGAGACCGCGGCCGTTATACTCACGACCCCTACCGTGTCA
CGCCCAAAACGGCGCTGGTGGTGTGTCGCGGAGTGCAACCCGCAACCGAGTGTGTCGCGGATCCGCGGACCAATCC
CGCACCCAGTCGCCAAACCCGAAATCACCGTGATGCCGTGGTAACTGACACCGACAGTAACGTCACTACGGCCGCC
ACGCCGACGCCGAACCAACGACGACATGATGATCGGCTG (SEQ ID NO. 89)

Clone Rv145

:::Rv145SP6.seq:::

ATATTCAACCTTGCACACATTGACGATACCTTGGTCACGAGACCCCAAAGCTGGCCTCCACCGCGCGCCGGGGACCA
CGGTACATACCTTGANNNGCTTTTCGATCGTTGATGCTGCGTCTTGGTCCGCGGAAACCGCAGGCTGGCATATGCACGT
GGGCGCACTGGCGATCTGCGATCCCCACCGATTGCGCCGAATACAGCTTTCAGCGGCTCCCCAAGTTGATCATCGACC
GGCTGCCGGATATCCGCACTTGGCGTGGCGGGTACCAGCGCCCCGCTCGGACTGGACCGCCGTGGTTCGTCGAGG
ACCACGAAC (SEQ ID NO. 90)

:::Rv145T7.seq:::

CAGGCATGCAAGCTTCATGCCGCGGCATGATAGCCACATGCACGCAATCGAACTCAGCGAAACCGGCGGGCCAGGCG
TCTTACGCCACCTCACCAGCGCGCAACCTCAACCGGCCACGGAGACCTCCTGATC (SEQ ID NO. 91)

Clone Rv146

:::Rv146SP6.seq:::

ATACTCAAGCTTGATTTTGATCATCATGATGATCATCAACCGAATTGTGGTAGCCGCACTGGTTATCGTGGGTACCGT
CGTGCTTTCCATGGGCGCCTCTTTCGGGCTTTCCGTATTGGTCTGGCAGGACATTCTGGGTATCGAGTTGTACTGGAT
GGTGTGGCGATGTCGGTGATCCTGCTCNTGGCGGTGGGATCCGACTACAATCTGCTGCTGATTTCCCGGTTGAAAGA
GGAAATTGGGCGCGGATTGAACACCGGAATTATCCGTGCCATGGCTGGTACCGGGGAGTGGTGACGGCTGCCGGCAT
GGTGTTCGCGTTACCATGTCGTTGTTGTGTTTCAGCGATTTGCGAATTATTGGTCAGATCGGTACCACCATCGGCCT
GGGCTTGCCTGTTTCGACACCCTCGTCGTGCCTCGTTCATGAAACCGTCCATTGCTGCCCTGCTGGGACCTGGTTCTGGT
GGCCGCTACGGGTGCGCCGCGCCCGGCACTCAATCTTCCGCCG (SEQ ID NO. 92)

:::Rv146T7.seq:::

CAGGCATGCAAGCTTGGCGTGCCGTTCCAACCGAATTGGCTTTTCGGCGCCATCGGTGAGGACGGCGTGCGGGTGCTC
AACGACGACGTCGTCCGCGGGACACACCTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTA
CAACGCCGCGCGGAACGCTTCCGCCGCGGGCGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGAC
GGCATCGCCACCGGAGCGACGGCCAAGGCGGCGTGCCAGGTGCGCCGCGCACGGTGCGGACAACGTGGTGCTGGCG
GTCCCCATCGGCCAGACGACATCGTGGCGAGA (SEQ ID NO. 93)

Clone Rv147

:::Rv147SP6.seq:::

ATACTCAAGCTTTTACGGTGATCGCGCATCACCTGGTTCATGAACTGGAAGCAGCGCAGCGCTTCCTTTTCGGCCGCA
ACATGAGCCAGCCTCTCGTCGGCGGTGCGGTGACAGGTGCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCTGAAAC
CAGCTTCCATATCCCGCGACGAACGACGCCAGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACAGCGCGTT
CTCCACCGACCGGGCCCGGGTGTGGGTGTTTCGGCGACCGGCACCCANGTGGTCCACACTGCCGAAG

(SEQ ID NO. 94)

:::Rv147T7.seq:::

TAGTCGCTGACCGGTGCAGGTTTCGACNATGTGGTGCCGTTTCGGCGGCTACGTGCCATCGAGACACTGGCGCAGGCT
ATCGCACCCGTTATCGGCTACGAGCAAATCGCGGTATGCGTTCCTGAGCATGAGTCGGCGACCGTCTCATGGTCGAC
ACCCACGACGGAAGACGAGATCGCCGCTTANCNTGTGTGCCGCGGATTATCAGGACTGACCTCCTGGCTGACCGGC
ATGTTTGGTCGCGATGCCTGGCGCCCGGCGGCGTGGTCTGGTGGCTCGG (SEQ ID NO. 95)

Clone Rv148

:::Rv148SP6.seq:::

ATACTCAAGCTTTCCGCCGATACCGGCATGTCGCGCACATCCAGAACTTCTGGGGGGATCCGCTGACAGCGGCGGGA
TCCCAAAGTGCGGATGATCGGGCCGCTACGTGCTGGTGTACCTCGTCCGTAACAACGAAACCGAAGCGTATGACTCG
GTCCACGCGGTGCGGCACATGGTGGACACCACCGCCACCGCAGGGGTGAAGGCCTATGTACCGGTCCGGCAGCA
CTCAATGCCGACGAGCCGAGGCGGAGACAAAAGTATCGTAAGGTACCGCGATCAGGACATGGTGATCGCAGCA
ATGTTGCTAGTGATCTATCGCCCCGTAATTACCGCGGTTCTCGTCTTGATCATGGTCGGCATCGACCTCGGCGCAATC
CGCGGATTNCTCGCTTGTGCTCGCCGACCACAACATTTTCAGCCTTTCAACATTTGCGACAACCTGCTCGTTCTCATGG
CGATTGCNGCGAAC (SEQ ID NO. 96)

:::Rv148T7.seq:::

CAGGCATGCAAGCTTGGCGTGCCGTTCCAACCGAATTGGCTTTTCGGCGCCATCGGTGAGGACGGCGTGCGGGTGCTC
AACGACGACGTCGTCCGCTGGACACACCTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTA
CAACGCCGCGCGGAACGCTTCCGCCGCGGGCGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGAC
GGCATCGCCACCGGAGCGACGGCCAAGGCGGCGTGCCAGGTGCGCCGGGCGCACGGTGCGGACAAGGTGGTGCTGGCG
GTCCCGATCGGCCAGACGACATCGTGGCGAGATTCCCGGGTACGCCGATGAAGTGGTGTGTTTGGCGACCGGCG
TTGTT (SEQ ID NO. 97)

Clone Rv149

.....Rv149SP6.seq.....
ATACTCAAGCTTTGGCATTGTGCACATTTCCACCCGCTGCTCTATTAATGCTGAGCCGCTAATTGTGACCCAGTCGG
GAAACACGCGGAGCACAAATTCACCGCAGCGCGGGGGCGGTTCAACTCACCATGGATCGCTCTCGTCGTCTGGTGC
TGGACAATCGTCGCTGTAGCGCGTCGCGAACACCTCAGCTTCTGCTGCCGCGGCTTCTCCGGCGATGGTAACCCCA
GGTTTCGCCCACGGTCTTACGTAGCAGTGCGACGCGGTGTTTCATCTGCATCGACCTGTTGACTCATCCTGTCAAGGAT
GAAGGCGTACTGGGCGGACTGCGCCTTCTGCCGCGCCAGGTCGGCAATCACCAGGATCTCAGAACGAGCTGCGACTC
ACTCTTCCAGGCCACCTGGCCGAAAGCTCGACATGGTCAATCCGGCCG (SEQ ID NO. 98)

.....Rv149T7.seq.....
CAGGCATGCAAGCTTGCGGGCGGAGTGGTTTCGACGGCGGCTCGCTTCTCGGCATCGGTTTGGGCTGTCAACAGCAG
TTGGTAGTTCTTCACGTACTGTTGTCGAGCGTCGAGCCGCGCGCTGTGAGGTCGCCGGACGCGTATCCCGCCAG
GCCGGTCAGGGTGCCCTTCCAGTCCACGCGCTGTGGTCGGCGAACCCTTATCTTCAATCGAGACGATCGCCAGCTT
CATCGTGTGGCGATCTTGTCCGAGGCGACCTCGAACCGCGCTGCGAGTACAGCCACGCGATCGTGTGCCCTTCG
GTCGACCATCGTCGATACCGCAGGCACTTGCCCTC (SEQ ID NO. 99)

Clone Rv14

.....Rv14SP6.seq.....
ATACTCAAGCTTCCCGGCGGCCAGTACCGAAAGCGCGAACAGCTCGCGGCAGCCACGACGTGCTGCGTCGGATTGCC
GGCGGCGAAATCAATTCCAGGCAGCTCCCGGACAAATGCGGCTCTGCTGGCCCGCAACGAAGGACTCGAGGTACCCCG
GTGCCGGGGTCTGTTGTCACCTGCCGATCGCACAGGTTGGCCACAACCGGCCGCTTGATGCCCGGTGCGCAAGCCC
GGCAGTTGCCAAACCCAGCGTGATCAGGCTCGGCTCGCGAGTTGCGCGAAGAAGTGGCTCGCCTGATCACCTACCATC
GGCCAGGATCTGCGTGTATCACAACGCTCGCCCAAGGAGTTGTTGTTGCTATCGACGGCCTTTAGCCAGATGTTT
GGAATCGACTATCCGATAGTGTCCGCGCAATGGACTTGATCGCCG (SEQ ID NO. 100)

.....Rv14T7.seq.....
AGCTTCGGTGTAGCCGATCACCGGAAGCCGCATGATCAGCCACGTTTCGCGCCGCCCGGCATACGGCGGCGTACCGAT
CTCCGCGTCATACACCCGCGGTAATCGCCGACGGTGCCGGTTCGCGAGCCGAAGGTGACGACGCTGATTGAATCGAG
TTCCAGGTCCAGCGGGTGGCGCAGCAACGGCGCGAGCTCAACGACGTCATCAGTTGTCGCTTCTACGGTCACCGA
CCCGGTGACCGTAGTCGCGCGGTGCGCTCGGCCGAGAAGTTGACCGGCCACCACCGCGACACCGCTTTGACGCGGAC
GCCACCCCGGATCGGTTGTGGCCAAGTAATTGGGTATTCCATTTGACGGGACGCCGACCCCGCAGCCCCAGTAC
CGCCACGACACGCGCGGTGACCCACCACTGTACGAACACCAAGGCGACGCCGA (SEQ ID NO. 101)

Clone Rv15

.....Rv150SP6.seq.....
ATACTCAAGCTTCCGGTGGCTTCGCCC GCCCTGCCGGTGGACTTCATGACAACGCGGGGGCGATTACCCCGCTACCG
CCAGCAGCATGACGGCGGTACCTAACACCGCCCGGATGCCTCGACGTCCTCGATGTGCTCAGGAATCGCCCCGGC
ACCGCGATCTCGAGGATCACCAGCGTTACCCCGGCGAGCGGACACCGACAATTCGCTACCCGCCACGCCGATCCGG
CCCTGGGCCAGCTGATTGGAGCTGGCG (SEQ ID NO. 102)

.....Rv150T7.seq.....
CAGGCATGCAAGCTTCCACATGTACGGATCCACGAACATCCCGTTGAACTGACAGGTGCGGCGCGGCTCGATCAGGCC
GGCCAATTGTTCTACGCGGTTACCGAAGATCTCTTCGGTGACCTGCCCGCGCGGCCAGCTCGGCCCCAGTGCCCGGC
GTTGGCGCGCGCGGACGATCTTGGCGTCCACGGTGGTCCGGGTCTTGCCCGCTAGCACGATCCGCGAGTCGGCCGG
TCACCCGGGT (SEQ ID NO. 103)

Clone Rv151

.....Rv151SP6.seq.....
ATACTCAAGCTTCCAAGTCCCAAGTGTGATCATGGCCAAAGAGCTCGACAAAGCCGTAGAGGCGTTTCGGACCCGC
CCGCTCGATGCCGCGCCGTATACCTTCCTCGCCGCCGACGCCCTGGTGCTCAAGGTGCGCGAGGCGAGCCGCGTCGTC
GGGTGCACACCTTGATCGCCACCGCGCTCAACGCCGAGGGTACCGAAAGATCCTGGGCATCCAGGTCACCTCCGCC
GAAGACGGGGCGGCTGGCTGGCGTTCTTCCGCGACCTGGTCGCCCGCGGCTGTCCGGGTGCGCTGGTCAACAGC
GACGCCACGCCGCGCTGGTGGCCGCGATCGGGGCCACCTGCCCGCAGCGGCTGGCAGCGCT (SEQ ID NO. 104)

.....Rv151T7.seq.....
CAGGCATGCAAGCTTCAACGTAGGCGCGCTCGATAAATGACTCCGCCGCGCTTCGCACATCCTCGTAGCGATCCTTG
CGAGCAGGTCAACCGGGCGCTGCCGTCGAGGACCGGTTTTTGGCGTGCAGCCACTGGCCGACACCTCGGGGGGTA
AGCGAATCCGAGAGCAGGAGGACGAGGTACGGAAGCTCGCCGAGCCGGTCTACCGCTCAGGGCGGATGTGCGCGGT
CGCCACCCGCGTACCGCCGATCGGACACCTGTATGACCGCGCGACGTC (SEQ ID NO. 105)

Clone Rv152

.....Rv152SP6.seq:.....
CGCGGCGGCGCATTACCCCGCTACCGTCAGCAGCTTGACGGCGGTAGCGAACACCGCCGGATGCAGCGCAGGTGCGT
CTATGTGCACACGGAATCGCCCCGGCACC GCGATCTCGAGGATCACCAGTGCCCCCCCCCTG (SEQ ID NO. 106)

.....Rv152T7.seq:.....

GGGATCGAGGAACAGCGCGTTGAACTGATAGGTGCGGCCCGGCTCGAGCAGGCCGGCCATTTGTTGATGCGGTTACC
GAAGATCTCTTCGGTGACCTGCCCCGCCCGCGCCAGCTCGGCCAGTGCCCCGGCGTTGGCCGCCCGCGGCAGCATCTT
GGCGTCCACGGTGCTCGGGGTGATGCCCCGCGAGCAGGATCGGCGAGCGGCCGGTCAGCCGGGTGAACTTCGTTCGAGAG
CTTGACCTGCGGTGCGGGAGCGGAACACGGTCGGTGCGTATCTCGACCAGGCCCGGGCAACCTCGGGGGTGGCGCC
GACGGTGAACAGGTTGCGCTGGCCACCGCGGTAGCCGCCGGCACTATGCCGATGCCAGGCCGCGGATCACCAGGTGC
GGTCAGTCGGGTGAGGATGTGCCCCGGCCCCAGGTGGAAGATCCAGCGGGCGCGGCCGCGTGGACACNGGTGATCTC
GTCCACCATCGACTTTCTGATCA (SEQ ID NO. 107)

Clone Rv153

.....Rv153SP6.seq:.....

TAACTCAAGGCTTGCGTTGAGGCCCGAGGCCATCGACGGTTTGGCGGCCCTTAAATGCACTGAGGTGCTCAATTGACC
CCACAGCGGAAATGCCGACTATTCGACGGCCTCCTTCGCCTTGGCTGCCGGAGAGGGGCTCCGCGGGAACCGCATGCA
GGTATATGACCTCGGTTTCTCGGGTGCTACCGCGTGCTTGTGAGGATGAACTCGGCGTTGGAATTGTCCAGCCGGC
CCAATTTCATCGAGCGCAGATTGCTACACATGCCCCGGCGGCGACATACGCTTCACCGTGGATCTGCTCCACACGGACCG
CCCTGTGCGGATCCTGCTCACGGGTAAAGGAACTTACNTGGCNCTCGGTGCC (SEQ ID NO. 108)

.....Rv153T7.seq:.....

CCTTCTGCGCCACCCACACCGTCAACGCCCGCGAAGTCGACGTCGTCCAGGCCATCGGCGGCCCTCACGGATGGATTGCG
GCGCGGACGTGGTGATCGACGCCGTGCGGCCGACCGGAAACCTACCAGCAGGCCTTCTACGCCCGCGATCTCGCCGGAA
CCGTTGTGCTGGTGCGGTGTCGCCGACGCCGACATGCGCCTGGACATGCCGCTGGTCTGACTTCTTCTCTCACGGCGGTG
CGCTGAAGTCGTGCTGGTACGGCGATTGCTTCCGAAAGCGACTTCCCCACGCTGATCGACCTTGACCTGCATGGCC
GGCTGCCGCTGCAGCGGTTGTTTCCGAACGCATCGGGCTCGAAGACGTGAGGAGGCGTTCCACAAGATGCATGGCG
GCAAGGTATTGCGTTCGGTGGTGATGTTGTGATGGCCGCCATCGAGCGGTCATACCCACGG (SEQ ID NO. 109)

Clone Rv154

.....Rv154SP6.seq:.....

ATACTCAAGCTTGATTTGATCATCATGATGATCATACCCGAAGTGTTGAGCCGCGAGTGTTATCGTGGGTACCGT
CGTGCTTTCCATGGGCGCTCTTTTCGGGCTTTCCGTATTGGTCTGGCAGGACATTCTGGGTATCGAGTTGTAAGT
GGTGTGGCGATGTCGGTGATCCTGCTCCTGGCGGTGGGATCCGACTACAATCTGCTGCTGATTTCCCGGTTGAAAAA
AGAAATTGGGGCCGGATTGAACACCGGAATTATCCGTGCCATGGCTGGTACCGGGGGAGTGTTACCGCTGCCGGCAT
GGTGTTCGCCGTTACCA (SEQ ID NO. 110)

.....Rv154T7.seq:.....

ATTGNCTTTTCGGCGCCATCGGTGAGGACGGCGTGCGGGTGCTCAACGACGACGTCGTCCGCGGGACACACCTCGATGC
TGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGGAACGCTTCCGCCCGGGCGTGA
CCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGACGGCATCGCCACCGAGCGACGGCCAAGGCGGCGTG
CCAGGTGCGCCCGGGCGCACGGTGCGGACAAGGTGGTGCTGGCGGTCCCAGTCGGCCAGACGACATCGTGGCGAGATT
CGCCGGGTACGCCGATGAGGTGGTGTGTTTGGCGACGCCGCGGCTTGTCTTCGCCGTGCGGCAGGGTTACCGCAACTT
CACCCAGACCTCCGACGAAGAAGTGGTGGCGTTTTCTGGATCGTGCTC (SEQ ID NO. 111)

Clone Rv155

.....Rv155SP6.seq:.....

ATACTCAAGCTTTTCCCGTCCGTATCGCCCAAGCGCGTGAGGCCGAAGCGGCTGGTTACGACTCCCTGTTTGTGATG
GACCACTTCTACCAACTGCCCATGTTGGGGACGCCCGACCGCGATGCTGGAGGCCTACACGGCCCTTGGTGCGCTG
GCCACGGCGACCGAGCGGCTGCAACTGGGCGCGTTGGTGACCGGCAATACCTACCGCAGCCCGACCTGCTGGCAAAG
ATCATCACCACGCTCGACGTGGTTAGCGCCGGTCGAGCGATCCTCGGCATTGGAGCGGTTGGTTTGGAGCTGGAACAC
CGCCAGCTCGGCTTCGAGTTCGGCACTTTAGTGACCGGTTCAACCGGCTCGAANAGGCGCTACAGATCCTCGAGCCA
ATGGTCAAGGTGAGCGCCAACGTTTTTCGGCGATTGGTACCCACCGA (SEQ ID NO. 112)

.....Rv155T7.seq:.....

CGGCCACCGGGGCCACTCCGCACAATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTCGCCGACTTTC
CGCGGTACCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAATACTTTCATCC
TGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGACCCAGTACTACATCATTC

GCACGGAGAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGGTTCAAC
CAAACCTTGAAGGTGATTGTTAACCTGGGCTACGGCGACCCGGCCTATGGTTATTCGACCTCGCCGCCCAATGTTGCGA
CTCCGTTCCGGTGTTCCTCCAGAGGTACGCCCGGTGCTCATCGCCGACGCTCTCGTCGCCGGGACCAGCAGGGAATCGG
CGATTTCCGCTACA (SEQ ID NO. 113)

Clone Rv156

:Rv156SP6.seq::

ATACTCAAGCTTGGGGTGGCGCTGTCGGTGGTGTGCTTGGCGGCGTCGGTATCAACACCGCCACGAAATGGGGCAC
AAGAAGGATTCGCTGGAGCGGTGGCTGTCCAAAATCACCTCGCCAGACCTGCTACGGGCACTTCTACATCGAGCAC
AACCCTGGCCATCACNTCCGGGTGTCCACACCGGAGGACCCGGCGTCGGCGCGGTTCCGGCAAACGTTGTGGGAGTTC
CTGCCCCGCGAGTTATCGGCGGCTTGCCTCGGCCGTTTCATTTGGAGGCCCAACGGCTGCGTCGGCTCGGCGTCAGC
CCCTGGAATCCCATGACGTATCTGCGCAACGACGTGCNCAACNCGTGGCTGATGTCNGTGGTGTGTTGGGGTGGGC

(SEQ ID NO. 114)

:Rv156T7.seq::

TCCGACCCGACCGCGGCGAACGCTCAAAGGCACCTACTGGCACCAAGGCCCCACACGTCACCCTGTGACCTCCTGCG
CCGACCCCGCCCGAGGTCTTGGCCGTTACACCGAACGGGCGAGCCGGGAGTCTGGTACGCATCGAACAAGAGCAAG
GTGCATGGGCGGAGTTGTTCCGCCACTTCGTCGATGACGGGGTCGATCCATTGAGGTCCGTCGCCGCGTCGGTCGAG
TGGCGGTACACTCCAGGTACTCGACCTCACAGACGAGAGGACTCGATCCCATCTAGGTGTGGACGAAACAGATCTTC
TGTCCGACGACTACACCACCCAGGCCATCGCCGCGCCGCGATGCCAATTGACGCGCTACTGGCCCCGGCGG
CGGCGCTCCCGGTTGTCAAACACTTTGCCGTGTTGTTTACGCACTGCCAACATCGAGCCCGA (SEQ ID NO. 115)

Clone Rv157

:Rv157SP6.seq::

ATGAAATAAGAAGAGCACATCCCTCAGTCGGTTATCATCACTAGCGCTCGCCGACCCGTCGTAACCGATCATAGCGAG
CGAACTGGCGAGGAAGCAAAGAATATCTGTTCTGTGATAGCTCTTACGCTCAGCGCAAGAAGAAATATCCCCGCG
GGAACAACCTCCAGGTAGAGGTACACACGCGGATAGCCAATTGAGAGTAATAAACTGTGACACTCACACCCTCATCAAT
GATGACGAATACACCCCGATATCCGGTCACATGACGAAGGGAAAGAGAAGGATATCATCTGTGACAACTGCCCTCA
AATTTGGCTTCCTTAA (SEQ ID NO. 116)

Clone Rv159

:Rv159SP6.seq::

ATACTCAAGCTTGTGAACTCCTTCTGAATACCGGCCGGCCATCCACAGATGCCCGGAAGAACTTCCAGGTACCCAT
GGCGGCTGGATCAGGGGGCGGCACAGTTGGTCTTGTCTGCTCGAGTGGCGTCGTTGTCCGGCTTGGACGGGGCTCC
GACGGTACCGGAGGGCAGCGACAAAACACTTATGCACTTGGGCGACCCGCGAGACGGTCGACACCCATCCCGACGG
CACAAGCTCAGCCGCGGCGCTCTTGTCTTCGTCGGATCGACATTACCCACTTCTGACCGGGCTTGGGCGAAGGAA
GCAGAA (SEQ ID NO. 117)

:Rv159T7.seq::

GGTATAGTCGCTGACCGGTGCAGGTTTCGACAATGTGGTGCCGTTTCGGCGGCTACGTGCCATCGAGACACTGGCGCA
GGCTATCGACCCGTTATCGGCTACGAGCAAATCGCGGTATGCGTTCTTGAGCATGAGTCGGCGACCGTCGTCATGGT
CGACACCCACGACGGAAAGACGAGATCGCCGTCAAGCATGTGTCCGCGGATTATCAGGACTGACCTCCTGGCTGAC
CGGCATGTTTGGTCGCGATGCCTGGCGCCCGCGGCGTGGTCTGGTTCGGCTCGGATAGCGAGGTGAGCGAATTCTC
GTGGCAGCTCGAAAGGGTCTGCGGTCGCGGTCTTTGCGCAAACGATGGCGCAGGTTACGGTCGCGCGGGGTGCGGC
CCTGGCGGCGGCCA (SEQ ID NO. 118)

Clone Rv15

:Rv15SP6D2.seq::

GAACTATATNATACTCAAGCTTCAGGTCAATGTGCGCAAGCCCTGACGCTGGCCGACCAGGCCACCGCCGCGGAN
CCCTNTCTAGA (SEQ ID NO. 119)

:Rv15T7.seq::

CTGTAGCCACCTGTGCCATCCCGTCATGCCCGACTCTGGTTCATCTCGGATCCGCTGACACCCCGCTAAGGCTGCTC
CTCTCGGTGCATTACCTACCGACGGCGAACNCCCCAGCTTTACGACTATCCGGATGACGGCACCTGGTTGCCGGCT
AACTTCACCGTCAGCTTGGACGGCGGCGTACCGTCGATGGCGCCAGCGGGGCGATGGCCGGGCGCGGACCGGATTC
GTCNTCANCTGTGCGGTGAATTTGCCGACGTCATCGTGGTTCGGTGTGGGCAACGTCGCGATTGAGGGCTACTCCGGC
GTCCGGATGGGTGTCGTCAAGCGCCCGCACCGGCGAGGCCGA (SEQ ID NO. 120)